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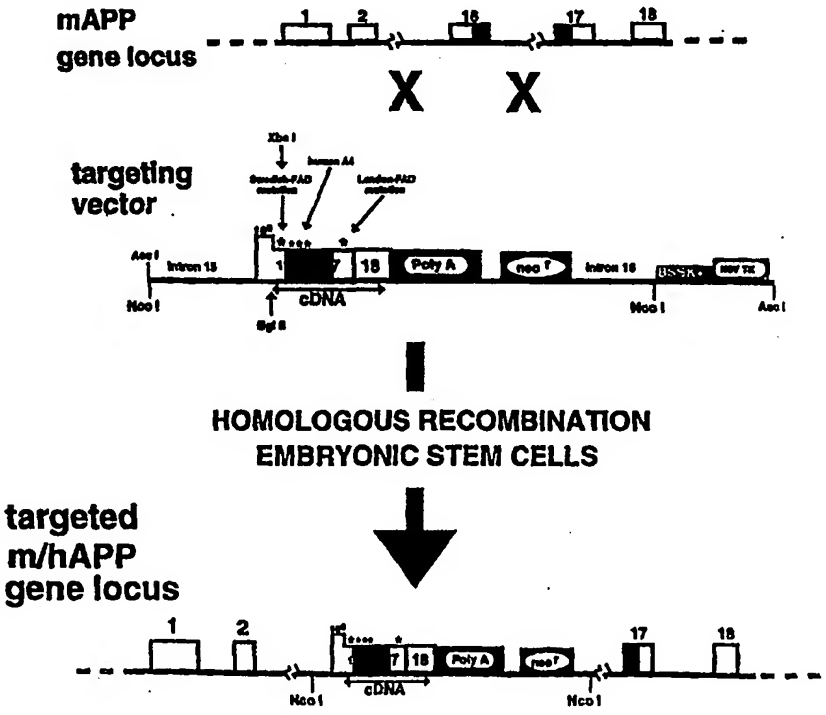
(54) Title: METHOD OF INTRODUCING MODIFICATIONS INTO A GENE

(57) Abstract

The present invention relates to a gene targeting vector and a method of using it to modify nucleic acid sequences. A gene targeting vector in accordance with the invention can comprise: a nucleotide sequence which is effective to achieve homologous recombination at a predefined position of a target gene, operably linked to the 5' terminus of a nucleotide coding sequence which, when inserted into a target gene, codes for at least one amino acid whose identity and/or position is not naturally–occurring in the target gene, and a nucleotide sequence which is effective to achieve homologous recombination at a predefined position of the target gene, operably linked to the 3' terminus of said nucleotide coding sequence. The nucleotide coding sequence can code without interruption for an amino acid sequence, where the amino acid sequence is coded for by two or more exons in a naturally–occurring gene.



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METHOD OF INTRODUCING MODIFICATIONS INTO A GENE

BACKGROUND

The current prior art methods of modifying genes are cumbersome and difficult. For example, mutagenesis of the mouse gene locus via "hit-and-run" and "tag-and-exchange" gene targeting technologies can require the mouse gene locus to be targeted two times in succession using the same ES cell clone. This is a long and laborious process. It is extremely difficult to maintain totipotency of the ES cell through so many manipulations and over such long periods of time in culture. To overcome the difficulties in the prior art, we have developed a novel method of targeting and engineering gene sequences.

The current state of the art provides for three different approaches to the development of transgenic animal models (Lamb, *Nat. Genet.*, 9:4-6, 1995). The first approach utilizes pronuclear injections of recombinant minigenes into the pronuclei of 1-cell embryos. In the second approach, a complete gene residing in yeast artificial chromosomes (YACs), is electroporated into embryonic stem cells (ES cells). The third approach utilizes gene targeting techniques in ES cells to introduce point mutations into a gene present in the ES cell chromosome. The most common approaches to introducing point mutations are "hit-and-run" (Hasty et al., *Nature*, 350:243-246, 1991) or "tag-and-exchange" (Askew et al., *Mol. Cell. Biol.*, 13:4115-4124, 1993), (Stacey et al., *Mol. Cell. Biol.*, 14:1009-1016, 1994) gene targeting procedures.

Recombinant minigenes, when injected into mouse embryos, integrate into the mouse chromosome at random locations. The site of integration can often exert a deleterious influence on the pattern of expression and/or expression level of the recombinant level of the recombinant minigene ("position effect") (Bonnerot et al., *Proc. Natl. Acad. Sci.*, 87:6331-6315,

1990; Brinster et al., *Proc. Natl. Acad. Sci.*, 85:836-840, 1988; Grosveld et al., *Cell*, 51:976-985, 1987).

To illustrate the benefit and ease of the novel compositions, methods, treatments, etc., described herein, we have utilized genes associated with Alzheimer's disease. Therefore, although aspects of this disclosure are written with respect to Alzheimer's diseases, e.g.,the APP gene, it is recognized that this invention is in no way limited to such genes and diseases, but may be applied to any nucleic acids, etc., that one desires to target and/or modify.

Alzheimer's disease (AD) is a neurodegenerative disorder characterized by progressive deterioration of memory and cognition. Prominent histopathological features of this disease include the extracellular deposition of amyloid and the accumulation of intracellular neurofibrillary tangles. The principal underlying cellular features of AD are the degeneration affects many types of neurons and may account for the numerous neurological deficits that patients afflicted with the disease encounter. The most notable degeneration occurs in the hippocampus, cerebral cortex, and amygdala, regions of the brain that play a major role in memory, cognition, and behavior.

Although numerous attempts have been made to generate transgenic mouse models for AD via the pronuclear injection approach (Lamb, 1995), only one line of transgenic mice has succeeded in developing extra-cellular plaque-like deposits of beta-amyloid (Games et al., *Nature*, 373:523-527, 1995). This transgenic mouse line utilizes the PDGF promoter to over-express (> 10 fold) human "London"-FAD APP. Because of the artificial nature of the transgene's regulation of gene expression and the aberrant high levels of APP expression, the accumulation of amyloid in this line of transgenic mice may not be fully relevant to the cellular mechanisms involved in Alzheimer's disease.

Two additional papers report only partial success in developing AD-like pathology. In one transgenic model, human APP 751 is over-produced in the brain using the brain-specific enolase promoter (Higgins et al., *Ann. Neurol.*, 35:598-607, 1994). This mouse model exhibits diffuse extra-cellular staining for beta-amyloid, but there was no evidence of accumulations of plaque-like deposits as described by Games et al. (Games et al., 1995). Another transgenic model exhibits intra-cellular deposits of beta-amyloid (La Ferla et al., *Nat. Genet.*, 9:21-30, 1995). This deposition leads to neuropathological processes, including apoptotic neurons and gliosis.

All transgenic mice derived via pronuclear injections retain the ability to express mouse APP. It has been demonstrated that mouse amyloid peptides do not aggregate in solution nearly as well as the human amyloid peptides (Dyrks et al., *FEBS Lett.*, 324:231-36, 1993). It is likely that the mouse amyloid peptide interferes with the process of human amyloid aggregation. This may, in part, explain the necessity in the existing mouse AD model to greatly over-express human amyloid in a mouse brain to develop extra-cellular amyloid deposits.

The human APP gene locus encompasses a very large region (~400 Kb). Transgenic mice have been generated using YACs which appear to contain an intact human APP gene (Lamb et al., 1993; Pearson and Choi, *Proc. Natl. Acad. Sci.*, 30:10578-10582, 1993). But because gene regulatory elements have been identified at considerable distances from the proximal promoter of many genes (e.g., (Grosveld et al., 1987) and (Simonet et al., *J. Biol. Chem.*, 268:8221-8229, 1993)) there is no assurance that a given APP YAC clone contains all necessary APP gene regulatory elements. AD is a complex disease of aging, and the regulation of APP gene expression may play a critical role in the onset and progression of the disease. An accurate mouse model for AD may very well require the presence of critical APP gene regulatory elements which may be missing or altered in the YAC clones. In

addition, the YACs will integrate at random sites in the mouse chromosome after electroporation and expression of the human APP gene may be altered in a detrimental fashion due to "position" effects (see above).

YAC clones are inherently unstable and it can be very difficult to generate transgenic mouse lines where the gene locus resident on the YAC has remained intact. Furthermore, FAD mutations need to be introduced into the very large YACs via homologous recombination in yeast. Determining the stability and integrity of FAD-APP YACs require considerable effort (Lamb et al., 1993, Pearson and Choi, 1993).

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to a method of modifying a target nucleic acid. The target nucleic acid preferably comprises a genomic DNA sequence. The invention also relates to recombinant nucleic acid molecules which comprise a nucleotide sequence effective for homologous recombination at a predefined position of a gene and which is operably linked to a nucleotide coding sequence. Such recombinant nucleic acid molecules can be further combined with a vector sequence, a selectable marker, etc., to form a targeting vector useful for modifying a target nucleic acid, e.g., a genomic DNA sequence. The invention also relates to transgenic animals which comprise cells containing a recombinant gene, e.g., an APP gene or a presenilin gene, where the gene has been modified or engineered using the mentioned gene targeting vector. The transgenic animals are useful as animal models for diseases associated with the modified gene locus, e.g., Alzheimer's disease for the APP or presenilin genes.

An object of the invention is a novel gene targeting strategy that facilitates the introduction of one or more specific mutations into any gene in a single double reciprocal homologous recombination step, providing a clear advantage over other gene targeting approaches which use at least two

transfection and screening/selection steps. The gene targeting strategy preferably utilizes double reciprocal homologous recombination and a positive selectable marker gene to facilitate the insertion of gene segments or cDNA's (from the same or a heterologous host) into specific sites within the chromosome of a desired host cell, e.g., an embryonic stem (ES) cell derived from a rodent such as mouse. By the term "cDNA", it is meant a DNA which has been obtained by copying mRNA. The gene segments or cDNA's can be modified to encode one or more mutations. These gene-to-gene segments or gene-to-cDNA fusions, therefore, allow the introduction of one or more specific mutations into the coding sequence of the targeted gene. For some purposes, it may be preferable to employ a cDNA which is modified by the addition of other desired sequences, either coding or non-coding.

An aspect of the invention is a recombinant nucleic acid molecule comprising a nucleotide coding sequence, e.g., a cDNA, which is operably linked at its 5' or 3' terminus, or at both, to a nucleotide sequence which is effective to achieve homologous recombination. The invention also relates to a nucleotide sequence of a rodent APP gene such as a murine APP gene, or other mammal, which is effective to achieve homologous recombination at a predefined position in a target gene, operably linked to the 5' terminus, 3' terminus, or both, of a nucleotide sequence coding for at least one amino acid which is not naturally occurring at a specific amino acid position of the target gene. When the molecule comprises sequences at its 5' and 3' terminus which are homologous to the target gene, the molecule is effective to achieve homologous recombination with the target gene located, e.g., on a chromosome.

The term recombinant means a nucleic acid molecule which has been modified by the hand-of-man, e.g., comprising fragments of nucleic acid from different sources or a nucleic acid molecule from one source which has been engineered. Thus, the nucleic acid molecule is recombinant, e.g.,

because it comprises nucleotide sequences from a rodent (e.g., mouse) gene and a human gene or a synthetic (i.e., engineered) nucleotide sequence. Homologous recombination is a process in which nucleic acid molecules with similar genetic information line up side by side and exchange nucleotide strands. A nucleotide sequence of the recombinant nucleic acid which is effective to achieve homologous recombination at a predefined position of a target gene therefore indicates a nucleotide sequence which facilitates the exchange of nucleotide strands between the recombinant nucleic acid molecule at a defined position of a target gene, e.g., a mouse APP gene. The effective nucleotide sequence generally comprises a nucleotide sequence which is complementary to a desired target nucleic acid molecule (e.g., the gene locus to be modified), promoting nucleotide base pairing. Any nucleotide sequence can be employed as long as it facilitates homologous recombination at a specific and selected position along the target nucleic acid molecule. Generally, there is an exponential dependence of targeting efficiency on the extent or length of homology between the targeting vector and the target locus. Selection and use of sequences effective for homologous recombination is described, e.g., in Deng and Capecchi, *Mol. Cell. Bio.*, 12:3365-3371, 1992; Bollag et al., *Annu. Rev. Genet.*, 23:199-225, 1989; Waldman and Liskay, *Mol. Cell. Bio.*, 8:5350-5357, 1988.

The nucleotide sequence effective for homologous recombination can be operably linked to a nucleotide sequence, preferably comprising a nucleotide coding sequence, which is to be recombined into the desired target nucleic acid. For example, an aspect of the present invention is to replace all or part of the amino acids comprising exons 16, 17, and 18 of the APP gene with a cDNA coding for all or part of the corresponding amino acids of a human APP gene. This is achieved by attaching a part of the APP gene comprising a part of intron 15 and exon 16 to the 5' terminus of a human cDNA and a part of the APP gene comprising a part of intron 16 to the 3'

terminus of the cDNA to form a targeting vector. The APP gene segments are positioned with respect to the human cDNA in a way such that homologous recombination between them and the mouse gene will result in replacement of exons 16 through 18 with the cDNA. Such positioning, i.e., operable linkage, means that the mouse gene segment is joined to the cDNA whereby the homologous recombination function can be accomplished.

A nucleic acid comprising a nucleotide sequence coding without interruption means that the nucleotide sequence contains an amino acid coding sequence for a polypeptide, with no non-coding nucleotides interrupting or intervening in the coding sequence, e.g., absent intron(s) or the noncoding sequence, as in a cDNA.

An object of the present invention is to introduce modifications into genomic sequences, e.g., by introducing into or replacing a genomic sequence with a cDNA. Such cDNA can comprise one or more mutations, thereby facilitating the introduction of any desired nucleotide sequence into a target nucleic acid. The introduced nucleic acid, e.g., a DNA can particularly encode modifications in, or which span, two or more exons of a desired gene using only a single, double reciprocal homologous recombination event. In one embodiment, two independent point mutations can be introduced into a genomic sequence, where each point mutation is located in a different exon of the same gene. Thus, the coding sequence can be a nucleotide sequence which codes without interruption for an amino acid sequence, where the amino acid sequence is coded for by two or more exons in a naturally-occurring genomic (i.e., gene) sequence. This includes, e.g., a coding sequence for an amino acid sequence which is a cDNA, where the cDNA comprises amino acids coded for by separate exons of a naturally-occurring genomic sequence comprising exons and introns. By the phrase naturally-occurring genomic sequence, it is meant the gene structure as it occurs in nature. For example, a human APP gene contains 18 exons in a

naturally-occurring form which has been described. See, e.g., Yoshikai et al., *Gene*, 87:291-292, 1990. Other gene structures are also possible.

The introduction of point mutations via a replacement type vector has been described (Rubinstein et al., *Nucl. Acid Res.*, 21:2613-2617, 1993). Rubinstein et al. did not consider fusing genomic sequences with cDNA sequences to encode the gene product. Therefore, the gene targeting technology described by Rubinstein et al. would not succeed in introducing the Swedish-London and Swedish-714 stop double mutations into the mouse APP gene locus. The beta-amyloid domain resides on two separate exons (Lemaire et al., *Nucleic Acid Res.*, 17:517-522, 1989; Kang and Muller-Hill, *Biochem. Biophys. Res. Comm.*, 166:1192-2000, 1990). While the Swedish mutation and human amino acid differences reside on exon 16, the London mutation resides on exon 17. Lambda genomic clones are not large enough to encompass both exons (Lamb et al., *Nature Genetics*, 5:22-30, 1993). Therefore, the introduction of the double mutations into a host gene locus (e.g., a mouse APP gene) by the previously described gene-targeting approaches would require multiple gene targeting events utilizing two independent targeting vectors. Thus, it is recognized that in accordance with the present invention mutations which span sequences too large to fit into conventional vectors, targeting strategies, etc. (such as described in Lamb et al., 1993), e.g., two or more exons, can be introduced into genomic DNA by preparing targeting vectors comprising an intron effective for homologous recombination and a contiguous coding sequence, e.g., from the two or more exons.

The nucleotide coding sequence can code for at least one amino acid whose identity and/or position is not naturally-occurring in a target gene, e.g., a rodent (e.g., mouse) or non-human mammal gene. This means that the nucleotide coding sequence, when inserted into the target gene such that an open reading frame is formed with the target gene coding sequences,

contains at least one non-identical amino acid from the coding sequence of the unmodified target gene. This can mean amino acid substitution, deletion, or addition. In the examples below which illustrate, but in no way limit the invention, a nucleic acid coding for amino acids of a mouse APP gene are replaced by nucleic acid coding for amino acids of a human APP gene. At least 5 alternative splice forms of APP have been detected (reviewed in Beyreuther et al., Ann. NY Acad. Sci., *695*, 91-102 (1993)). The amino acids of a human APP gene means amino acid(s) identified as non-identical when the two APP gene sequences are compared. The amino acid numbering in the patent application refers to the largest alternative splice form of APP which consists of 770 amino acids. See, e.g., Kitaguchi et al., Nature *331*, 530-532 (1988); Tanaka et al., Biochem. Biophys. Res. Commun., *157*, 472-479 (1988). For example, the human amino acid sequence differs in the beta-amyloid domain are at positions 676, 681, and 684. The mouse APP gene contains a glycine at amino acid position 676, and a phenylalanine at amino acid position 681, and an arginine at amino acid position 684. A nucleotide coding sequence, which when inserted into an open reading frame of the mouse APP gene, comprising an arginine at amino acid position 676, a threonine at amino acid position 681, and/or a histidine at amino acid 684 is considered to contain three amino acid(s) whose identify is not naturally-occurring at an amino acid position (i.e., 676, 681, and/or 684) in the target mouse APP gene. See Figure 17 for other differences between the mouse and human APP polypeptide sequence.

A nucleic acid coding for at least one amino acid not naturally occurring in the targeted gene can also comprise, e.g., nucleotides which occur in a naturally-occurring human gene, such as naturally-occurring polymorphisms, alleles, or mutations which are discovered or identified in a natural population. By the term naturally-occurring, it is meant that the nucleic acid is obtained from a natural source, e.g., animal tissue and cells,

body fluids, tissue culture cells, forensic samples. Any other amino acid(s) can be incorporated, as well as, e.g., conservative and non-conservative amino acid substitutions, amino acid(s) obtained from other genes, non-naturally-occurring or engineered sequences, functional and/or selectable coding sequence domains.

In the examples, a mouse APP gene is targeted by the substitution of an amino acid found in a human APP gene. Numerous naturally-occurring mutations have been identified in non-murine APP genes. A nucleic acid according to the present invention can contain such mutations. Other modifications to the sequence can comprise mutations found in familial or genetic cases of disease, preferably Alzheimer's disease, Down's syndrome, or heredity cerebral hemorrhage with amyloidosis Dutch type (HCHWA-D). A nucleotide sequence coding for all or part of an amino acid sequence of a human APP gene can contain codons found in a naturally-occurring gene or transcript, or it can contain degenerate codons coding for the same amino acid sequences.

Preferred human APP amino acid sequences include: Swedish-FAD, KM(670,671)NL; London-FAD, V(717)I; Swedish/London-FAD, KM(670,671)NL, V(717)I; stop codon at position 714; Swedish-FAD, KM(670,671)NL, stop codon at position 714, etc. See Table 1.

An amino acid sequence of a human APP gene comprising a nucleotide sequence to be inserted into a targeted mouse APP gene preferably codes without interruption and comprises arginine at 676, threonine at position 681, histidine at position 684, or combinations thereof, in addition to other mutations and engineered codons.

The present invention also relates to nucleic acids which hybridize to a nucleic acid coding for an amino acid sequence of a human APP gene, preferably under stringent conditions. Such hybridizable sequences are

preferably not a naturally-occurring mouse APP nucleotide sequence; however, mutant mouse APP sequences can be included.

Hybridization conditions can be chosen to select nucleic acids which have a desired amount of nucleotide complementarity with the nucleotide sequence coding for all or part of an amino acid sequence of a human APP gene. A nucleic acid capable of hybridizing to such sequence, preferably, possesses 50%, more preferably, 70% complementarity, between the sequences. The present invention particularly relates to nucleotide sequences which hybridize to the nucleotide sequence coding for human APP amino acids under stringent conditions. As used here, "stringent conditions" means any conditions in which hybridization will occur where there is at least about 95%, preferably 97%, nucleotide complementarity between the nucleic acids. A nucleotide sequence hybridizing to the coding sequence will have a complementary nucleic acid strand, or act as a template for one in the presence of a polymerase (i.e., an appropriate nucleic acid synthesizing enzyme), which has a corresponding amount of nucleotide identity or similarity. The present invention includes both strands of nucleic acid, e.g., a sense strand and an anti-sense strand. Thus, it is understood that a nucleic acid comprising a nucleotide sequence hybridizing to the coding nucleotide sequence of amino acids of a human APP gene also represents a nucleic acid which possesses at least about 95%, preferably 97% nucleotide sequence identity.

According to the present invention, at least one amino acid not naturally-occurring in the targeted gene also includes amino acids selected from engineered or non-naturally-occurring sequences. In the examples, a mouse APP gene is modified by replacing mouse amino acids with amino acids which naturally occur in a human APP gene. However, the mouse APP gene can also be modified or engineered by the introduction of amino acids which are not based on a human APP gene, e.g., conservative or non-

conservative amino acids, cysteines, prolines, functional and/or selectable domains, etc.

Changes or modifications to the nucleotide coding sequence can be accomplished by any method available, including directed or random mutagenesis to a nucleic acid. These sequence modifications include, e.g., nucleotide substitution which does not affect the amino acid sequence (e.g., different codons for the same amino acid), replacing naturally-occurring amino acids with homologous or conservative amino acids, e.g. (based on the size of the side chain and degree of polarization), small nonpolar: cysteine, proline, alanine, threonine; small polar: serine, glycine, aspartate, asparagine; large polar: glutamate, glutamine, lysine, arginine; intermediate polarity: tyrosine, histidine, tryptophan; large nonpolar: phenylalanine, methionine, leucine, isoleucine, valine. In addition, it may be desired to change the codons in the sequence to optimize the sequence for expression in a desired host.

In addition to a gene segment effective for homologous recombination and coding sequence to be recombined, e.g., a recombinant nucleic acid molecule according to the present invention also can include selection markers, 3' regulatory sequences, regulatory sequences, restriction sites, vector sequences, and sequences and/or modification which enhance homologous recombination.

In order to identify cells which have integrated the nucleic acid molecule, it is desirable to include a selectable marker gene, e.g., neomycin resistance, gene HPRT gene, etc. A selectable marker gene codes for a product which can be directly or indirectly detected in a host in which it is expressed. Selectable marker genes and their use are widely used in molecular biology. When a neomycin resistance gene is utilized, cells having incorporated it can be selected by resistance to G418. A second selectable marker gene can also be incorporated into the vector, e.g., a herpes simplex

virus thymidine kinase gene. Any selectable genes routinely used in host cells can be used in the gene targeting vectors, including HSV TK, neo^r, hygromycin, histidinol, Zeocin (Invitrogen), HPRT, etc. Selectable genes can also be included to select against random integration events. Thus, selection for the first marker (e.g., by positive selection), and absence of the second marker (e.g., by negative selection), permits enrichment for transformed cells containing a modified target nucleic acid sequence, e.g., at the APP gene locus. The choice and arrangement of the selectable marker gene(s) in the recombinant nucleic acid molecule are as the skilled worker would know, e.g., described in U.S. Pat. No. 5,464,764 and Rubinstein et al., *Nucl. Acid Res.*, 21:2613-2617, 1993. A preferred recombinant nucleic acid comprises a selectable marker gene, e.g., a gene for neomycin resistance, in the mouse APP gene segment 3' to the cDNA. The selectable marker genes can be operably linked to regulatory sequences which control their expression, e.g., in a cell or tissue specific manner. Examples of such sequences are described, e.g., in U.S. Pat. No. 5,464,764.

In accordance with the present invention, 3' regulatory nucleotide sequences can be operably linked to a recombinant nucleic acid molecule. For example, it may be desirable to include a transcription termination signal and/or polyadenylation signal (e.g., AATAAA tandem repeat) at the 3' end of the nucleotide sequence to be inserted into the foreign gene. Generally, a selectable marker gene directly follows the transcription, termination and polyadenylations signals. Other sequences can also be included, e.g., nucleotide sequences which regulate the stability of a mRNA.

A recombinant nucleic acid can also comprise nucleotide sequences which affect expression of the gene into which it is combined, e.g., enhancers.

A recombinant nucleic acid molecule according to the present invention can also comprise all or part of a vector. A vector is a nucleic acid

molecule which can replicate autonomously in a host cell, e.g., containing an origin of replication. Vectors can be useful to perform manipulations, to propagate, and/or obtain large quantities of the recombinant molecule in a desired host. A skilled worker can select a vector depending on the purpose desired, e.g., to propagate the recombinant molecule in bacteria, yeast, insect, or mammalian cells. Examples of useful vectors include Bluescript KS+II (Stratagene). The following vectors are provided by way of example, Bacterial: pQE70, pQE60, pQE-9 (Qiagen), pbs., pD10, phagescript, psiX174, pbluescript SK, pbsks, pNH8A, pNH16a, pNH18Z, pNH46A (Stratagene); ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 (Pharmacia). Eukaryotic: pWLNEO, pSV2CAT, pOG44, pXT1, pSG (Stratagene), pSVK3, pBPV, pMSG, pSVL (Pharmacia). However, any other vector, e.g., plasmids, viruses, or parts thereof, may be used as long as they are replicable and viable in the desired host. The vector can also comprise sequences which enable it to replicate in the host whose genome is to be modified. The use of such vector can expand the interaction period during which recombination can occur, increasing the targeting efficiency.

Recombinant nucleic acid molecules according to the present invention can also include sequences and modifications which decrease nonhomologous recombination events and/or enhance homologous recombination. For example, it has been found by Chang & Wislon, *Proc. Natl. Acad. Sci. USA*, 84:4959-63, 1987, that the addition of dideoxy nucleotides to the recessed termini of DNA molecules could enhance homologous recombination 6- to 7-fold relative to nonhomologous events.

Recombinant nucleic acid molecules according to the present invention can be prepared according to the various methods known to the skilled worker in the art, e.g., as mentioned in *Current Protocols in Molecular Biology*, Edited by F.M. Ausubel et al., John Wiley & Sons, Inc; and

Current Protocols in Human Genetics, Edited by Nicholas C. Dracopoli et al., John Wiley & Sons, Inc.

In accordance with the present invention, the novel gene-targeting can be used to modify any desired gene. Figure 15 illustrates several general strategies. Figure 15A shows a "typical" host gene with a DNA sequence consisting of a gene promoter, a series of exons (5 in this example). The exons are depicted as boxes. The gene can contain one or more exons. The line between the boxes (exons) represent the introns. The 5'-end of each intron contains a splice donor site which lies directly juxtaposed to the 3'-nucleotide to the preceding exon. The 3'-end of each intron contains a splice acceptor sequence which lies directly juxtaposed to the 5'-end of the neighboring exon. The 3'-end of the last exon contains a nonsense codon (designated as a stop) to terminate translation. This is followed by 3'-untranslated sequences which are present in the gene transcript and then a transcription termination and polyadenylation signal (designated polyA).

Figure 15B illustrates a targeted gene where a cDNA is inserted directly into an exon (exon 4 in this example) of the gene. Using an appropriately designed gene-targeting construct, any exon of a mouse gene can be targeted in this fashion. This is the approach used in the examples to generate the Swedish and/or London FAD-m/hAPP transgenic mice. The sequence of the cDNA is arranged so that the fusion between the gene and the cDNA creates an "in-frame" sequence that properly encodes the desired protein. The cDNA can be modified to encode one or more mutations (designated at *). The cDNA can be derived from transcripts from other genes of the same species or from genes from other species.

The cDNA is inserted into the mouse by homologous recombination. The recombination occurs between the targeted gene and an exogenously added gene-targeting construct or vector. The vector is preferably linearized. For homologous recombination to insert the cDNA into the proper location

and orientation within the targeted gene, the DNA components of the vector can be arranged in a specific manner. The cDNA is preferably positioned between nucleotide sequences which are homologous to specific locations of the targeted gene.

In the gene-targeting vector, there is preferably a gene segment comprising a nucleotide sequence corresponds substantially to an upstream (5'-flanking) region of the targeted gene. This segment comprises contiguous and sufficient upstream (5'-flanking) sequences of the targeted gene to allow efficient recombination to take place, i.e., a nucleotide sequence which is effective for homologous recombination. The segment can be followed by a portion of the targeted gene exon (exon 4 in this example).

In the gene-targeting vector, the sequence spanning the junction between the 3'-end of the targeted gene exon (exon 4 in this example) and the 5-end of the cDNA are arranged precisely in-frame to conserve the open reading frame to properly encode the desired gene product. In effect, the cDNA and the exon into which it is inserted become the terminal exon of the targeted gene. For proper termination and maturation of the transcript encoded by the targeted gene, transcription termination and polyadenylation signals (designated polyA) are positioned directly after the cDNA (and after the translation of stop codon). Directly following the transcription termination and polyadenylation signals, the gene targeting vector further comprises a selectable marker gene such as the neomycin resistance gene (designated neo^r) or the HPRT gene.

The gene targeting vector can further comprise a downstream (3'-flanking) region of homology to the targeted gene which is placed directly after the selectable marker gene, e.g., neo^r. The downstream region of homology can comprise contiguous gene sequences but can be any length of sequence providing it is sufficiently long to facilitate homologous recombination. The 5'-end of the downstream region of gene homology can

be located at any position proximal to the targeted gene as long as it lies downstream (3') of the mouse gene sequence which forms the junction between the targeted gene exon and the cDNA. After homologous recombination has taken place, the DNA sequence of the targeted gene positioned between the 3'-end of the upstream region of gene homology and the 5'-end of the downstream region of gene homology will have been deleted.

After homologous recombination takes place, exon sequences lying 5' of the exon/cDNA junction will encode the N-terminal portion of the gene product while the cDNA sequences lying 3' of the exon/cDNA junction will encode the C-terminal portion of the gene product.

Figure 15C illustrates a targeted gene where a cDNA is inserted directly into an intron (intron 3 in this example) of the targeted gene. Using an appropriately gene-targeting construct, any intron of a gene could be targeted in this fashion.

The sequence of the cDNA is arranged so that it functions as the terminal exon of the targeted gene. To form an open reading frame between the targeted and human coding sequence, the codon reading-frame of the cDNA sequence is positioned in-frame with the codon reading-frame of the nearest upstream (5') exon (exon 3 in this example). For proper splicing of messenger RNA to occur, a functional splice acceptor site immediately preceding (5') the cDNA can be included. Thus, after splicing of the exon with the cDNA, a resultant transcript from the targeted gene will encode the desired gene product. As mentioned above, a cDNA from various sources can be utilized and it can be modified to encode mutations. The arrangement of the gene targeting vector is as described above.

Figure 15D illustrates a targeted gene where a gene segment from another the same or different species (designated as foreign gene segment) is inserted directly into an intron (intron 3 in this example) of the targeted gene.

Using an appropriately gene-targeting construct, any intron of a gene can be targeted in this fashion. In this example, the sequence of the foreign gene segment contains normal exons and introns from another gene. The sequences of the gene-targeting construct are arranged such that the foreign gene segment functions as the terminal set of exons for the targeted gene. The codon reading-frame of the exons of the foreign gene segment can be arranged in-frame with the codon reading-frame of the nearest upstream (5') exon (exon 3 in this example) to form a complete open-reading frame. For proper splicing of messenger RNA to occur, a functional splice acceptor site immediately preceding the 5' exon of the foreign gene segment can be included. Thus, after splicing of the exon with the exons of the foreign gene segment, the transcript from the targeted gene will encode the desired gene product. The foreign gene segment can be obtained from various sources, as desired, and can be engineered to encode one or more mutations. The arrangement of a gene targeting vector is described above.

Another aspect of the present invention relates to host cells comprising a recombinant nucleic acid of the invention. A cell into which a nucleic acid is introduced is a transformed cell. Host cells include, mammalian cells, e.g., rodent, murine Ltk-, murine embryonic stem cells, COS-7, CHO, HeLa, insect cells, such as Sf9 and Drosophila, bacteria, such as E. coli, Streptococcus, bacillus, yeast, fungal cells, plants, embryonic stem cells (e.g., mammalian, such as mouse or human), neuronal cells (primary or immortalized), e.g., NT-2, NT-2N, PC-12, SY-5Y, neuroblastoma. See, also *Methods in Enzymology*, Volume 185, ed., D.V. Goeddel. A nucleic acid can be introduced into the cell by any effective method including, e.g., calcium phosphate precipitation, electroporation, injection, DEAE-Dextran mediated transfection, fusion with liposomes, and viral transfection. When the recombinant nucleic acid is present in a host cell, it is preferably

integrated by homologous recombination into a chromosome residing in the host cell.

The present invention also relates to a recombinant nucleic acid coding for a recombinant polypeptide, which nucleic acid is a product of the gene which has been modified by the gene targeting vector. A gene can code for different nucleic acid transcripts, depending on splicing, where it is expressed, etc. All such nucleic acids are a product of the recombinant gene and thus relate to the present invention. Such nucleic acids can code for recombinant polypeptides which are also an object of the present invention. The recombinant polypeptides can be used, e.g., as antigens to generate specific antibodies as diagnostic, research, and therapeutic tools.

A recombinant nucleic acid and a recombinant polypeptide can incorporate at least one amino acid or coding sequence thereof from a heterologous species. If, e.g., a non-human mammal sequence contains at least one amino acid of a human sequence, the modified sequence is described as "humanized." By "humanized" it is meant, e.g., a mouse polypeptide containing one or more amino acids which are present in the human polypeptide (and which differ from the amino acids present in the mouse gene).

Thus, in the examples, humanized mouse APP nucleic acids and polypeptides were created by substituting a human amino acid for a mouse amino acid at corresponding locations. A recombinant nucleic acid can be an unprocessed RNA transcript comprising introns or it can comprise a nucleotide sequence coding without interruption for amino acids, e.g., where the nucleic acid is a modified APP gene, it can code for amino acids 1-770, 1-713, 1-751, and 1-695. For example, a nucleic acid coding for a recombinant APP polypeptide can be a transcript from an APP gene modified in accordance with the present invention, e.g., by homologous recombination with a human cDNA and a mouse gene. The recombinant nucleic acid can

comprise mutations in the APP gene, e.g., Swedish-FAD, London-FAD, etc., as described above.

The present invention also relates to a non-human transgenic animal, preferably a mammal, more preferably a rodent such as a mouse, which comprises a gene, which has been engineered employing a recombinant nucleic acid according to the present invention. Generally, a transformed host cell, preferably a totipotent cell, whose endogenous gene has been modified using a recombinant nucleic acid as described above is employed as a starting material for a transgenic embryo. The preferred methodology for constructing such a transgenic embryo involves transformed embryonic stem (ES) cells employing a targeting vector comprising a recombinant nucleic acid according to the invention. A particular gene locus, e.g., APP, is modified by targeted homologous recombination in cultured ES cells employing a targeting vector comprising a recombinant nucleic acid according to the invention. The ES cells are cultured under conditions effective for homologous recombination. Effective conditions include any culture conditions which are suitable for achieving homologous recombination with the host cell chromosome, including effective temperatures, pH, medias, additives to the media in which the host cell is cultured (e.g., for selection, such as G418 and/or FIAU), cell densities, amounts of DNA, culture dishes, etc. Cells having integrated the targeting vector are selected by the appropriate marker gene present in the vector. After homologous recombination has been accomplished, the cells contain a chromosome having a recombinant gene. In a preferred embodiment, this recombinant gene contains host genomic sequences (e.g., mouse) fused to a donor cDNA (e.g., human). The cDNA can contain multiple mutations, etc., which are not naturally-occurring in the target gene. No further gene engineering steps are necessary. Thus, in accordance with the present invention, a single step has resulted in a modified gene containing as many modified sequences as

desired. Another aspect of the present invention involves employing a cDNA with sufficient nucleotide sequence dissimilarity between it and the native target gene sequence to avoid inappropriate intra-recombination and inter-recombination events, subsequent to the first gene targeting step.

The transformed or genetically modified cells can be used to generate transgenic non-human mammals, e.g., rodents (such as mice or rats), by injection into blastocysts and allowing the chimeric blastocysts to mature, following transfer into a pseudopregnant mother. See, e.g., *Teratomacarcinoma and Embryonic Stem Cells: A Practical Approach*, E.J. Robertson, ed., IRL Press. Various stem cells can be used, as known in the art, e.g., AB-1, HM-1 D3, CC1.2, E-14T62a, preferably ES cell line G1 derived from inbred mouse strain 129/SvEvT.

In accordance with the present invention, a transformed cell contains a recombinant gene integrated into its chromosome at the targeted gene locus. A targeting vector which comprises sequences effective for homologous recombination at a particular gene locus, when introduced into a cell under appropriate conditions, will recombine with the homologous sequences at the gene locus, introducing a desired gene segment (e.g., a cDNA) into it. When recombination occurs such that insertion results, the nucleic acid is integrated into the gene locus. The gene locus can be the chromosomal locus which is characteristic of the species, or it can be a different locus, e.g., translocated to a different chromosomal position, on a supernumerary chromosome, on an engineered "chromosome," etc. In the examples described below, the sequences of the human APP gene are integrated by homologous recombination into the normal APP gene loci on murine chromosome 16. By recombinant, it is meant that the nucleotide sequences come from different sources, e.g., mouse and human.

A transgenic non-human mammal comprising a recombinant gene, which when mutant results in Alzheimer's disease, can express the gene in an

amount effective to produce neuronal cell degeneration and/or apoptosis. The gene can also be expressed in an amount effective to cause a behavioral or cognitive dysfunction, wherein the dysfunction is conferred by the recombinant gene. Such gene can be, e.g., PS1, PS2, S182 (e.g., Sherrington et al., *Nature*, 375:754-760, 1995), STM2, E5-1, apoliprotein E, apoptosis genes such as ALG-1 to -6 (Vito et al., *Science*, 271:521, 1995), Bcl-2/Bax gene family, etc.

A transgenic non-human animal according to the present invention can comprise one or more genes which have been modified by genetic engineering. For example, a transgenic animal comprising an APP gene which has been modified by targeted homologous recombination in accordance with the present invention can comprise other mutations, including modifications at other gene loci and/or transgenes, including PS1, PS2, S182 (e.g., Sherrington et al., *Nature*, 375:754-760, 1995), STM2, E5-1, apoliprotein E, apoptosis genes such as ALG-1 to -6 (Vito et al., *Science*, 271: 521, 1995), Bcl-2/Bax gene family, etc. Modifications to these gene loci and/or introduction of transgenes can be accomplished in accordance with the methods of the present invention, or other methods as the skilled worker would know, e.g., by pronuclear injection of recombinant genes into pronuclei of one-cell embryos, incorporating an artificial yeast chromosome into embryonic stem cells, gene targeting methods, embryonic stem cell methodology. See, e.g., U.S. Patent Nos. 4,736,866; 4,873,191; 4,873,316; 5,082,779; 5,304,489; 5,174,986; 5,175,384; 5,175,385; 5,221,778; Gordon et al., *Proc. Natl. Acad. Sci.*, 77:7380-7384 (1980); Palmiter et al., *Cell*, 41:343-345 (1985); Palmiter et al., *Ann. Rev. Genet.*, 20:465-499 (1986); Askew et al., *Mol. Cell. Bio.*, 13:4115-4124 (1993); Games et al. *Nature*, 373:523-527 (1995); Valancius and Smithies, *Mol. Cell. Bio.*, 11:1402-1408 (1991); Stacey et al., *Mol. Cell. Bio.*, 14:1009-1016 (1994); Hasty et al.,

Nature, 350:243-246 (1995); Rubinstein et al., *Nucl. Acid Res.*, 21:2613-2617 (1993).

A recombinant nucleic acid molecule according to the present invention can be introduced into any non-human mammal, including a rodent, mouse (Hogan et al., *Manipulating the Mouse Embryo: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1986), rat, pig (Hammer et al., *Nature*, 315:343-345, 1985), sheep (Hammer et al., *Nature*, 315:343-345, 1985), cattle or primate. See also, e.g., Church, *Trends in Biotech.* 5:13-19, 1987; Clark et al., *Trends in Biotech.* 5:20-24, 1987; and DePamphilis et al., *BioTechniques*, 6:662-680, 1988.

A transgenic non-human animal and a recombinant nucleic acid molecule according to the present invention is useful as described in U.S. Pat. Nos. 5,304,489, 5,221,778, 5,175,385, 5,175,384, 5,175,383, 5,087,571, 5,082,779, 4,736,866, 4,873,191, and other transgenic animal patents. For example, a recombinant nucleic acid molecule comprising a coding sequence for at least one amino acid of a human APP gene is useful as a hybridization probe for detecting and diagnosing Alzheimer's disease, e.g., nucleotide variations and genetic polymorphisms present in a nucleic acid can be detected in accordance with various methods, e.g., U.S. Pat. 5,468,613; Conner et al., *Proc. Natl. Acad. Sci.* 80, 78 (1983); Angelini et al., *Proc. Natl. Acad.*, 83, 4489 (1986); Myers et al., *Science*, 230, 1242 (1985). The nucleic acid can also be operably linked to an expression control sequence to produce polypeptide encoded by it. The operable linkage of nucleic acid and expression control sequence can be introduced into a desired host, and cultured under conditions effective to achieve expression of a polypeptide coded for the nucleic acid. An expression control sequence is similarly selected for host compatibility and a desired purpose, e.g., high copy number, high amounts, induction, amplification, controlled expression. Other sequences which can be employed, include, enhancers such as from

SV40, CMV, inducible promoters, neuronal specific elements, or sequences which allow selective or specific cell expression, such as in neuronal cells, glial cells, etc. The expression control sequence includes mRNA-related elements and protein-related elements. Such elements include promoters, enhancers (viral or cellular), ribosome binding sequences, transcriptional terminators, etc. An expression control sequence is operably linked to a nucleotide coding sequence when the expression control sequence is positioned in such a manner to effect or achieve expression of the coding sequence. For example, when a promoter is operably linked 5' to a coding sequence, expression of the coding sequence is driven by the promoter. The resulting polypeptides can be used to generate antibodies for diagnostic purposes, etc. The operable linkage with an expression control sequence can also occur *in situ* as a result of homologous recombination at the desired gene locus, e.g., a mouse APP gene.

A further aspect is the expression of a modified mRNA and polypeptides encoded by a recombinant nucleic acid molecule of the present invention in a transgenic animal, preferably a non-human mammal, as a model for diseases associated with the gene, e.g., the APP, PS1, and PS2 genes with Alzheimer's disease (AD), Down's syndrome, and heredity cerebral hemorrhage with amyloidosis Dutch type (HCHWA-D). Expression of a modified gene product in a transgenic non-human mammal and its consequent phenotype can therefore be used as a model for diseases and pathologies, e.g., as an AD model for genes associated with Alzheimer's disease. As described in the examples below, a mouse APP gene is modified by the introduction of mutations which are associated with an Alzheimer's phenotype in humans. Transgenic mice comprising cells which contain such a modified or recombinant APP gene can be used to design therapies. For example, active agents, e.g., synthetic, organic, inorganic, or nucleic acids based molecules, can be administered to a transgenic non-human mammal

according to the present invention to identify agents which either inhibit, prevent, and/or reduce the appearance of an Aβ peptide in the brain, the AD pathology, neurodegeneration, apoptosis, cognitive deficits, and/or behavioral symptoms, etc. Thus, another aspect of the invention is to provide a method to assist in the advancement of the treatment and/or prevention of the aforementioned symptoms (e.g., neurodegeneration or apoptosis) caused by the APP gene, or a fragment thereof. Other genes and therapies can be used analogously.

Such a mammal model can also be used to assay for agents, e.g., zinc, and factors, e.g., environmental, which exacerbate and/or accelerate the diseases. See, e.g., Bush et al., *Science*, 265:1464-1467, 1994. A transgenic non-human animal can also be useful as pets, food sources (e.g., mice for snakes), in toxicity studies, etc.

Moreover, a non-human mammal containing a recombinant nucleic acid according to the present invention can be used in a method of screening a compound for its effect on a phenotype of a mammal, preferably a mouse, where the phenotype is conferred by the recombinant nucleic acid. By "phenotype," it is meant, e.g., a collection of morphological, physiological, biochemical, and behavioral traits possessed by a cell or organism that results from the interaction of the genotype and the environment. A phenotype can be behavioral, e.g., occurrence of seizures or cognitive performance, or it can be physiological and/or pathological, e.g., occurrence of neuronal cell degeneration, neuronal cell apoptosis, accumulation of Aβ peptide in the brain of the mammal, altered carboxy-terminal processing of the APP polypeptide, etc. According to such a method of detection, a compound can be administered to a mammal containing a modified APP gene and then the existence of an effect on the phenotype of the mammal can be determined. Observation can be accomplished by any means, depending on the specific phenotype which is being examined. For example, the ability of a test

compound to suppress a behavioral phenotype can be detected by measuring the latter phenotype before and after administration of the test compound.

The invention also relates to a transgenic non-human mammal comprising cells that contain a recombinant gene modified by a gene targeting vector. For example, such recombinant gene or nucleic acid can code for a humanized mouse polypeptide comprising at least one amino acid coded for by a human gene, e.g., where the gene is the APP, PS1, or PS2 gene. In the case of the APP gene, the gene can code for, e.g., amino acids 1-665 of a mouse APP gene and amino acids 666-770 of a human APP gene, and having a phenotype conferred by the modified gene, e.g., accumulation of Aβ peptide or other related peptide in the brain, abnormal processing of the APP polypeptide, etc.

The level of expression of the recombinant gene can be any amount which can produce a phenotype in the non-human mammal, which phenotype can be distinguished from mammals which do not possess the modified gene locus, i.e., a control mammal, e.g., an amount effective to produce neuronal cell degeneration and/or apoptosis and/or an amount effective to cause a behavioral and/or cognitive effect or dysfunction where the gene is an alzheimer's disease associate gene.

A non-human mammal containing a modified APP gene can also be characterized by accumulation of the Aβ peptide in its brain. The accumulation can be in any quantity which is greater than that observed in mammals not containing the modified gene locus. The phenotype conferred by the modified APP gene can occur before or after accumulation can be detected. The expression and/or accumulation of the APP polypeptide, and its processed derivatives, and the nucleic acids which encode it, can be measured conventionally, e.g., by immunoassay or nucleic acid hybridization, either *in situ* or from nucleic acid isolated from host tissues.

The identification of agents which prevent and/or treat symptoms associated with expression of the modified gene can be determined routinely. For example, an active agent can be administered to a transgenic mammal comprising a modified gene according to the present invention and then its effect on a behavior or pathology, e.g., Aβ deposition in the brain, apoptosis, and/or neurodegeneration, can be determined. The agent can be administered acutely (e.g., once or twice) or chronically by any desired route, e.g., subcutaneously, intravenously, transdermally, or intracathically. The formulation of the agent is conventional, see, e.g., *Remington's Pharmaceutical Sciences*, Eighteenth Edition, Mack Publishing Company, 1990. In a test, e.g., an agent can be administered in different doses to separate groups of transgenic mammals to establish a dose-response curve to select an effective amount of the active agent. Such effective amount can be extrapolated to other mammals, including humans.

The transgenic mammal, preferably a mouse, according to the present invention therefore permits the testing of a wide variety of agents and therapies. In AD, for example, a number of different agents have been identified which affect the cognitive dysfunction associated with the diseases, e.g., cholinergic agents, such as muscarine agonists, acetylcholinesterase inhibitors, acetylcholine precursors, biogenic amines, nootropics, angiotensin converting enzyme (ACE), and vitamin E. In addition, agents which regulate APP or Aβ expression, Aβ deposition, and physiological changes associated with Aβ expression and deposition can also be identified, e.g., calcium homeostasis, inflammation, neurofibrillary tangles. See, e.g., Pavia et al., *Annual Reports of Medicinal Chemistry*, 25:2129, 1989; John et al., *Annual Reports of Medicinal Chemistry*, 28:197-203, 1993. Additionally, active agents which block apoptosis, e.g., free radical scavengers, such as glutathionines, can be administered. Such effects on AD can be assayed in either behavioral or physiological and/or histological studies.

For example, spatial learning and memory abilities in mice can be tested in a Morris water maze. See, e.g., Yamaguchi et al., *NeuroReport*, Vol. 2, 781-784 (1991). Additionally, other behavioral tests can be used, e.g., Swim Test, Morris et al., Learning and Motivation, 12, 239-260, 1981; Open-field test, Knardahl et al., *Behav. Neurol. Biol.* 27, 187-200, 1979; and tests and models used routinely, e.g., in mice, rats, and other rodents.

According to the present invention, differences in, e.g., levels of expression, cellular localization, and/or onset of expression of the recombinant gene can be used to model a disease, e.g., AD and other diseases associated with APP expression and the differing stages and progressions of the disease, e.g., cell degeneration, cell death, astrogliosis, and/or amyloidosis. Having a range of expression phenotypes can be useful to identify different therapies and drug treatments and also diagnostically to identify a disease's progression. For example, the specific treatments can depend on the region of the brain in which an APP peptide is expressed, how much of it is expressed, and its temporal progression of expression. Thus, mammals having different phenotypes can be used as models for determining therapies which are selective for different stages of the disease and for studying disease progression and intervention.

DESCRIPTION OF THE FIGURES

Figure 1. Schematic of p35A; mouse APP exon 16 genomic clone

The ~15 Kb Not I genomic fragment (shown) was isolated from the lambda clone 35A and cloned into the Not I site of Bluescript II SK+. Exon 16 is indicated and begins approximately 9.5 Kb from the 5'-end of the genomic fragment. The indicated restriction enzyme recognition sites were placed for reference.

Figure 2. Restriction Map pMTI-2396

pMTI-2396 contains mouse APP exon 16 and was derived from the ~5.5 Kb NcoI fragment from p35A (NcoI at position 7645 to NcoI at position 13176, Figure 1). The 5.5 Kb NcoI fragment was inserted into NcoI-modified Bluescript II SK+ at the NcoI site. All recognition sites for the indicated restriction enzymes are designated. Sequence from positions 29 to 5560 were derived from the mouse APP gene and the remaining sequences were derived from Bluescript II SK+.

Figure 3. Restriction map of pRA3

pRA3 contains mouse APP intron 15 sequences and was derived from the ~3 Kb NcoI fragment from p35A (NcoI at position 4816 to NcoI at position 7645, Figure 1). The 3 Kb fragment was inserted into NcoI-modified Bluescript II SK+ at the NcoI site. All recognition sites for the indicated restriction enzymes are designated. Sequence from positions 29 to 2858 were derived from the mouse APP gene and the remaining sequences were derived from Bluescript II SK+.

Figure 4. Restriction map of pN2C4

pN2C4 contains mouse APP intron 16 sequences and was derived from the ~1.9 Kb NcoI fragment from p35A (NcoI at position 13176 to NcoI at position 14992, Figure 1). The ~1.9 Kb fragment was inserted into NcoI-modified Bluescript II SK+ at the NcoI site. All recognition sites for the indicated restriction enzymes are designated. Sequence from positions 29 to 1845 were derived from the mouse APP gene and the remaining sequences were derived from Bluescript II SK+.

Figure 5. Restriction map of pMTI-2398; Swedish-FAD targeting vector

The mouse APP intron 15 and exon 16 sequences encompass positions 30 to 1960 (BglII site). The human APP cDNA and genomic polyadenylation sequences are contained in sequences between positions 1960 and ~4556. The neomycin resistance gene lies between positions ~4556 and ~6460. Mouse APP intron 16 sequences are contained between positions ~6460 and 9872. The Bluescript II SK+ sequences are between positions ~9872 and ~30. All recognition sites for the indicated restriction enzymes are designated.

Figure 6. Restriction map of pMTI-2453; London-FAD targeting vector

The HSV TK gene is located between positions ~17 and ~2893. The mouse APP intron 15 and exon 16 sequences encompass positions ~2906 to 4835 (BglII site). The human APP cDNA and genomic polyadenylation sequences are contained in sequences between positions 4835 and ~7452. The neomycin resistance gene lies between positions ~7452 and ~9323. Mouse APP intron 16 sequences are contained between positions ~9323 and 12750. The Bluescript SK+II sequences are between positions ~12750 and ~37. All recognition sites for the indicated restriction enzymes are designated.

Figure 7. Restriction map of pMTI-2454; Swedish/London-FAD targeting vector

The HSV TK gene is located between positions ~17 and ~2893. The mouse APP intron 15 and exon 16 sequences encompass positions ~2906 to 4835 (BglII site). The human APP cDNA and genomic polyadenylation sequences are contained in sequences between positions 4835 and ~7452. The neomycin resistance gene lies between positions ~7452 and ~9323. Mouse APP intron 16 sequences are contained between positions ~9323 and 12750. The Bluescript II SK+sequences are between positions ~12750 and ~37. All recognition sites for the indicated restriction enzymes are designated.

Figure 8. Restriction map of pMTI-2455 (Swedish-FAD APP713 targeting vector)

The HSV TK gene is located between positions ~17 and ~2893. The mouse APP intron 15 and exon 16 sequences encompass positions ~2906 to 4835 (BglII site). The human APP cDNA and genomic polyadenylation sequences are contained in sequences between positions 4835 and ~7452. The neomycin resistance gene lies between positions ~7452 and ~9323. Mouse APP intron 16 sequences are contained between positions ~9323 and 12750. The Bluescript II SK+ sequences are between positions ~12750 and ~37. All recognition sites for the indicated restriction enzymes are designated.

Figure 9. Oligonucleotides

Oligonucleotides are designated in the 5' to 3' direction.

Figure 10. Schematic outline of m/hAPP gene products produced in transgenic mouse lines.

The protein m/hAPP exhibits amino acid sequence identity with mouse APP with the exception of those residues indicated by (asterisks, see text above). m/hAPP protein spans the membrane once as indicated. The bA4 peptide region (indicated by red) partially resides in the transmembrane and extracellular domains. The APP751 alternative splice form of APP has the 56 amino acid Kunitz protease inhibitor domain while the APP770 splice form of the protein has both the Kunitz and the 19 amino acid OX domains. The APP695 alternative splice form of APP contains neither Kunitz nor OX domains. Other splice forms are not indicated. There are two possible N-linked glycosylation sites (CHO) in the extracellular domain of APP. A highly negatively-charged domain and a cysteine-rich domain are symbolized by a minus sign and S-S bridges respectively. The signal peptide (SP) is located at the N-terminus (see Unterbeck et al.).

Figure 11. Gene-targeting strategy: Construction of targeting vectors.

The schematic of the Nco I APP gene fragment represents the ~5.5 Kb NcoI mouse APP gene fragment in pMTI-2396 (Figure 2). The regions indicated in red represent the coding sequences for mouse b-amyloid domain. The schematic for the targeting vector represents the linearized (using AscI) DNA from clone pMTI-2454 (Figure 7). The targeting vectors for pMTI-2453 (Figure 6) and pMTI-2455 (Figure 8) are identical to pMTI-2454 with the exception of the FAD mutation and the orientation of the HSV TK gene (see text). pMTI-2398 is similar to pMTI-2454 with the exception of FAD mutation and the absence of the HSV TK gene (see text). The FAD mutations are indicated by black asterisks and the mutations to "humanize" the b-amyloid domain are indicated by green asterisks. The neomycin resistance gene is designated by neo^r and Bluescript II SK+ sequences are designated by BSSK+.

Figure 12. Gene-targeting strategy: Homologous recombination.

The linearized targeting vector (Figure 11) was electroporated into ES cells. Homologous recombination occurred between mouse APP sequences contained in the targeting vector and mouse APP genomic sequences on chromosome 16. The resulting targeted m/hAPP gene locus is schematically shown. The FAD mutations are indicated by asterisks and the mutations to "humanize" the b-amyloid domain are indicated by asterisks.

Figure 13. Gene-targeting strategy: Targeted m/hAPP gene locus.

The comparison of the mouse APP and targeted m/hAPP gene loci is shown schematically. In normal mouse, the b-amyloid, transmembrane, and cytoplasmic domains of APP are encoded by mouse APP exons 16, 17, and 18. In the case of the targeted m/hAPP gene locus, the b-amyloid, transmembrane, and cytoplasmic domains of m/hAPP are encoded by human cDNA sequences. The remainder of m/hAPP is encoded by mouse APP exons 1 through 15. The FAD mutations are indicated by asterisks and the mutations to "humanize" the b-amyloid domain are indicated by asterisks.

Figure 14. Strategy for Southern-blot detection of ES cells having a targeted m/hAPP gene locus containing the Swedish-FAD mutation (e.g.; transgenic lines ES5007 and ES5103).

The schematics for the mouse and m/hAPP loci are indicated. The restriction enzymes XbaI and NcoI are designated by X and N respectively. The box represents human APP cDNA and genomic sequences while the box represents the neomycin resistance gene.

Figure 15. Gene Targeting Strategies

A. Normal Gene

B. Targeted gene. Fusion of a gene with cDNA (in-frame fusion of mouse exon sequences with cDNA). * represents one or more mutations.

C. Targeted gene. Fusion of a target gene with cDNA (cDNA is inserted into a mouse intron (intron 3 for example). The cDNA is directly preceded by a splice acceptor site. The sequence of the insert is formatted so that splicing of the 3'-sequence of the exon (exon 3 for example) with the 5'-sequence of the cDNA will create a mature transcript encoding the appropriate gene product). * represents one or more mutations.

D. Targeted gene. Fusion of a targeted gene with a foreign (same or different species) gene segment including one or more exons inserted into the intron of the targeted gene. The sequence of the insert is formatted so that splicing of the 3'-sequence of the mouse exon (exon 3 for example) with the 5'-sequence of the other mouse gene or species exon (exon 4' for example) will create a mature transcript encoding the appropriate gene product). * represents one or more mutations.

Figure 16. Amino acid sequence of human APP.

Figure 17. Sequence of mouse exon 16 locus

Figure 18. Sequence of pMTI-2398 (Swedish-FAD APP targeting vector)

Figure 19. Sequence of pMTI-2453 (London-FAD APP targeting vector)

Figure 20. Sequence of pMTI-2454 (Swedish/London-FAD APP targeting vector)

Figure 21. Sequence of pMTI-2455 (Swedish-FAD APP713 targeting vector)

Figure 22. Sequence of APP genomic clone containing human APP polyadenylation signals.

EXAMPLES

Four independent lines of transgenic mice (lines ES5007, ES5103, ES5401 and ES5403) have been created via a novel gene targeting technique applied to embryonic stem cells. In each line, the mouse APP gene has been modified to encode a mouse/human hybrid APP (m/hAPP) where amino acid residues 666-770 of APP770 are now encoded by human cDNA sequences instead of mouse genomic exons (exons 16, 17, and 18). Within these residues only three amino acid differences exist between the mouse and human proteins (Gly(676) to Arg, Phe(681) to Thr, and Arg(684) to His). This exon-cDNA fusion gene, therefore, encodes an APP containing a "humanized" beta-amyloid domain (aa residues 672 to 712).

In each transgenic mouse line, the human cDNA sequences have been modified to introduce one or more mutations proximal to the "humanized" beta-amyloid domain. In transgenic mouse line ES5007, m/hAPP has been mutated to include the "Swedish"-FAD mutation (KM to NL, positions 670 and 671)(Cai et al., 1993, Citron et al., 1994). Transgenic mouse lines ES5401 and ES5403 encode m/hAPP which have been mutated to include the "London"-FAD mutation (V to I, position 717) (Suzuki et al., 1994, Gravina, 1995). Transgenic mouse line ES5103 encodes m/hAPP which has been mutated to include both "London" and "Swedish" FAD mutations. A fifth transgenic mouse line ES5215 can be produced which encodes m/hAPP that has been mutated to include both the "Swedish" FAD mutation and a premature stop codon (T to stop at position 714). With the exception of the changes mentioned above, the remainder of the m/hAPP sequences are identical to those found in normal mouse APP.

We have shown that the targeted Swedish-FAD m/hAPP and Swedish/London-FAD m/hAPP genes express m/hAPP protein at levels approaching those observed for mouse APP in brain.

Notably, we have observed that the Swedish FAD mutation alters significantly the proteolytic processing of APP resulting in differences in the appearance of C-terminal fragments. The observed changes in processing is consistent with the Swedish-FAD mutation inducing the beta-secretase cleavage site to be utilized predominately over the alpha-secretase cleavage site as previously observed in cell culture experiments (see below).

Messenger RNA from the Swedish-FAD m/hAPP gene was found be abundantly expressed in the brain from homozygous ES5007 mice as well. The amount of Swedish-FAD m/hAPP mRNA in homozygous ES5007 brain was determined to be approximately 55% of the mAPP mRNA levels observed in control mouse brain. In concordance, the APP mRNA levels in heterozygous ES5007 mouse brain were found to be approximately 75% of the level observed in control mouse brain.

The reverse transcriptase-PCR (rtPCR) technique was used to identify mouse APP and Swedish-FAD m/hAPP transcripts in mouse brain. Homozygous ES5007 mice were found to express mRNA exclusively from the targeted Swedish-FAD m/hAPP gene. No mRNA species containing sequences from mouse APP exons 16, 17, or 18 was detected in homozygotes. As would be expected, heterozygous ES5007 mice were found to express mRNA transcripts from both normal mouse and Swedish-FAD APP alleles.

Western-blot analyses have demonstrated that Swedish-FAD m/hAPP and Swedish/London-FAD protein is expressed in the brain of ES5007 and ES5130 mice, respectively. Swedish-FAD m/hAPP protein is expressed in the brain of homozygous ES5007 mice at approximately 87% of the level observed for mouse APP in non-transgenic mice (n = 4).

Retrieving mouse APP exon 16 from genomic library

Phage lifts: The mouse 129 genomic library from Stratagene (cat#946308) was titered and plated out 20 150 mm LB plates containing ~50,000 phage/plate. Duplicate lifts were made from each plate using Amersham Hybond-N+ nylon membranes. The plates were refrigerated for several hours to ensure the top agar was hardened. The membranes were placed atop the plaques and left on for 5 minutes. The membranes were lifted off the plates and placed plaque-side up on 3MM paper saturated with denaturation solution (0.1 M NaOH, 1.5 M NaCl) for 5 minutes. The membranes were transferred briefly to dry 3MM paper to absorb the excess solution and then placed on 3MM paper saturated with neutralizing solution (0.2 M Tris-Cl pH 7.5, 2X SSC) for 5 minutes. The membranes were rinsed by placing them on 3MM paper saturated with 2X SSC for 5 minutes and then air dried. A digoxigenin-labeled mouse specific APP exon 16 probe of 93 bp was generated using PCR (from nt 1877 to 1969 in sequence MUSABPPA, accession #M18373).

PCR assay: In a 50 μl total reaction volume was added 1 μg genomic mouse tail DNA, 5 μl 10X PCR buffer (Perkin Elmer cat#N808-0006), 5 μl 2 mM dATP, dCTP, dGTP mix, 5 μl 1.3 mM dTTP, 3.5 μl 1 mM digoxigenin-11-dUTP, 3 μl 100 ng/ml oligonucleotide mix of KC65 (5'GTTCTGGGCTGACAAACATC3') and KC66 (5'GATGGCGGACTTCAAATCCTG3'), and 2.5 units AmpliTaq (Perkin Elmer cat#N808-0070). The reaction was run in a Perkin Elmer turbo 9600 thermal cycler. The parameters of the run were as follows: one cycle at 94°C for one minute, 36 cycles at 94°C for 30 seconds-56°C for 50 seconds-70°C for two minutes, maintain at 10°C indefinitely. Four individual PCR reactions were pooled and passed through a Sephadex G-50 column from Boehringer-Mannheim (cat#100616) in 10 mM Tris-Cl pH 7.5, 1 mM

EDTA, and 0.1% SDS. Several dilutions of the dig-labeled probe were blotted onto a membrane and compared to standard amounts of a dig-labeled control DNA.

Hybridization of plaque-lifted membranes: Membranes were pre-hybridized in 50% formamide, 5X SSC, 0.1% N-lauryl sarcosine, 0.02% SDS, and 5% blocking reagent supplied by Boehringer-Mannheim (cat#1096176) and incubated at 42°C for 4 hours. The pre-hybridization solution was discarded and replaced with identical fresh hybridization solution that contained 2 μg of the dig-labeled mouse APP exon 16 probe that was boiled for 10 minutes and chilled on ice. Membranes were hybridized over a two-day period at 42°C. All incubations (and heated-washes) were performed in the Stovall "Belling Dancing" water bath. The probe/hybridization solution was removed and saved for subsequent screenings. Membranes were washed four times in 2X SSC, 0.1% SDS at room temperature for 5 minutes. Subsequent washings were as follows: two washes of 30 minutes at 65°C in 0.5X SSC, 0.1% SDS; two washes for 30 minutes at 65°C in 0.2X SSC, 0.1% SDS; ten minutes at 65°C in 0.2X SSC; and ten minutes at room temperature in 0.2X SSC.

Digoxigenin detection assay: The remaining protocol is taken from the Boehringer-Mannheim "DIG Nucleic Acid Detection Kit" (cat#1175041). Membranes were rinsed once for 2 minutes at room temperature in Genius 1 buffer (100 mM Tris-Cl, pH 7.5, 150 mM NaCl) and blocked for 1 hour at room temperature in Genius 2 buffer (2% w/v blocking agent in Genius 1 buffer). Membranes were incubated with 150 μunits/ml of polyclonal sheep anti-digoxigenin alkaline phosphatase conjugated antibody in Genius 2 buffer for 30 minutes at room temperature. Two washes were done for 15 minutes each at room temperature in Genius 1 buffer and once for 2 minutes in AP

9.5 buffer (100 mM Tris-Cl pH 9.5, 100 mM NaCl, 50 mM $MgCl_2$). Membranes were processed in Lumi-Phos 530 (Boehringer-Mannheim cat#1275470) and placed in the dark for 16 hours then exposed to film for 20 minutes.

Positive plaques were picked and placed into 1 ml SM buffer (5.8 g NaCl, 2.0 g $MgSO_4 \cdot 7H_2O$, 50 ml 1 M Tris-HCl pH 7.5 to a total volume of one liter) to diffuse and stored at 4°C. These plaques were screened in a PCR assay using the identical oligonucleotide pair that was used to generate the probe (assay-15 μl phage stock and 35 μl water were heated to 95°C for 20 minutes into which was added 10 μl 10X PCR buffer, 3 ml 100 ng/ml oligo mix of KC65 and KC66, 10 μl 2 mM dNTP mix, 5 units AmpliTaq, and 1 unit Perfect Match Polymerase Enhancer (Stratagene cat# 600129) to a total volume of 100 μl).

Secondary membrane screenings on 4 isolates were performed using the digoxigenin-mouse APP exon 16 probe previously made. Two positive phage plaques were grown (protocol taken from BioTechniques 7:21-23) to obtain enough DNA for further analysis.

A 15 Kb sequence containing the mouse APP exon 16 was sub-cloned into pBluescript IISK+ (Stratagene cat#212205) at the NotI site (designated as plasmid 35A) using standard cloning procedures. Southern analysis using a 32p-labeled mouse APP exon 16 probe revealed a 5 Kb NcoI fragment which became the backbone into which our human APP cDNAs were fused.

Southern analysis: Six separate reactions containing 1 μg of plasmid 35A were digested with 10 units each of restriction enzymes ApaI (cat#114S), ApaI/BglII (cat#144L), NcoI (cat#193L), NcoI/BglII, XbaI (cat#145S), XbaI/BglII (supplied by New England Biolabs) in their respective buffers (total volume of 30 μl) at their respective incubation temperatures for 3 hours. One-half of the digestion reactions was loaded onto an 0.8% agarose

(Bio-Rad cat#162-0133) gel in 1X TBE buffer. The gel was run at 20 volts overnight at room temperature. After photographing the gel, it was prepared for transferring to a nylon membrane. The gel was soaked in 0.25N HCl, rocked gently, for 15 minutes, rinsed well with water then soaked in 0.4N NaOH, rocked gently, for 20 minutes. A 3MM paper wick transfer was assembled using Amersham Hybond-N+ nylon membrane in 0.4N NaOH buffer overnight at room temperature. The membrane was rinsed in 5X SSC for 10 minutes at room temperature and UV cross-linked in a Stratalinker (Stratagene cat. #400071) using $1.2x10^5$ mjoules for 30 seconds. The membrane was hybridized in 50% deionized formamide, 5X SSC, 0.1% N-lauryl sarcosine, 0.02% SDS, and 5% blocking agent (Boehringer-Mannheim) at 42°C, rocked gently, and incubated overnight. This solution was removed and replaced with the previously made mouse APP exon 16 digoxigenin-labeled probe (denatured) in fresh hybridization buffer and incubated at 42°C, rocked gently, for overnight. All subsequent washes, blocking, and antibody binding was identical to the protocol stated previously as digoxigenin detection assay.

Construction of the targeting vectors

Subcloning mouse exon 16 locus: The 5 Kb NcoI fragment containing the mouse APP exon 16 sequence was cloned into pBluescript IISK+ at an engineered NcoI site to generate pMTI2396 (Figure 2; see below). The 3 Kb 5'-flanking NcoI fragment and 2 Kb 3'-flanking NcoI fragments from p35A were also cloned into pBluescript IISK+ at the engineered NcoI site to generate pRA3 and pN2C4, respectively (Figures 3 and 4; see below). The pBluescript vector (1 μg) was digested with 20 units of XbaI in buffer 2 (NEB) and incubated for 2 hours at 37°C. Ten units of calf intestine alkaline phosphatase (CIP from Boehringer-Mannheim cat#713023) were added to the reaction and incubated for 1 hour at 37°C to dephosphorylate the 5' ends. To

500 ng of the 5Kb NcoI fragment was added 6.2 pmol of phosphorylated, annealed adapter KC95/96 (5'CTAGACACTC3') using 400 units of T4 DNA Ligase (NEB cat#202L) in its appropriate buffer (50 mM Tris-Cl pH 7.8, 10 mM $MgCl_2$, 10 mM DTT, 1 mM ATP 25 mg/ml BSA) at 25°C for a 5-hour incubation. This reaction was digested with 20 units of XbaI and adjusted the buffer concentration to 50 mM NaCl and incubated for 1 hour at 37°C. The enzyme was heat inactivated at 65°C for 20 minutes. The DNA was removed from the residing enzymes using Strataclean resin (Stratagene cat#400714). To the 25 μl enzyme digestion reaction was added 5 μl of Strataclean resin, vortexed for 15 seconds and set at room temperature for 1 minute. It was then spun in an Eppendorf microcentrifuge 5415C at 14000xg for 1 minute. The supernatant was transferred to a clean tube and the procedure was repeated once. Dephosphorylated XbaI-linearized pBluescript, 50 ng, was combined with 500 ng of the phosphorylated 5Kb NcoI-adapter fragment in a standard ligation reaction and incubated at 14°C for overnight. The ligase was heat inactivated at 70°C for 10 minutes and one-tenth of the reaction was transformed into Epicurian.coli XL-1 blue cells (Stratagene cat#200236) using the protocol provided. The resulting construct having mouse genomic sequences for the 3' end of intron 15-exon 16-5' end of intron 16 was then referred to as p2396 (Figure 2). The BglII site within exon 16 is the point at which the human cDNA sequence was fused.

Subcloning of NcoI fragments proximal to the Exon 16 targeting site: The 3 Kb intron 15 fragment and the 2 Kb intron 16 fragment were generated by a NcoI digestion on the template plasmid 35A (see Figure 1). The 3Kb and 2 Kb NcoI-NcoI fragments were then subcloned into the Bluescript (NcoI) vector (see above). The resulting plasmids were named pRA3 (3 Kb fragment; Figure 3) and pN2C4 (2Kb fragment; Figure 4). They were expanded and the 2 and 3 Kb fragments themselves isolated by Geneclean

(Bio 101). These isolated fragments were then used as probes in Southern blot paradigms.

Generation of cloning sites around the neomycin resistance gene: As an integral part of our targeting vector construct, we cloned the neomycin resistance gene (pPol2longneobpA provided by Ann Davis) downstream of our human APP cDNA sequence. The neomycin resistance gene (contained within a pBluescript KS+ vector) was under transcriptional regulation of the DNA polymerase II promoter sequence (long version) and the bovine growth hormone (BGH) polyadenylation sequences. Sequences composed of different restriction sites had to be cloned onto both the 5' and 3' ends of this gene construct. The plasmid, 2 μg, was linearized with SalI, ligated to 45 pmol of annealed SalI-AflII-EcoRV-NcoI-MluI adapter (5'TCGACGACTTAAGTTGATATCCACCATGGTGACGCGTT3') using 400 units of T4 DNA Ligase in its appropriate buffer at 14°C in an overnight incubation. This reaction was digested with EcoRV (cat#195S) and ligated to close. This plasmid, now referred to as p2395, was digested with XhoI to linearize it at the 3' end of the BGH sequence. Ligated to this XhoI site was an XhoI-BglII-StuI adapter (5'TCGAGTGAGATCTTAAGGCCTGG3'). The ligase was removed from the reaction using the Wizard DNA clean up system (Promega cat#A7280) following the directions supplied in the kit. The linearized plasmid-adapter DNA (approx. 5 μg) was digested with 30 units each, in one 50 μl reaction, of StuI (cat#187L)/EcoRV in restriction enzyme buffer 2 (from NEB) at 37°C for 3 hours. The digest reaction was run through a 0.8% low melt agarose (FMC cat#50112) gel in 0.5X TAE buffer (20 mM Tris acetate, 0.5 mM EDTA) at 75V for 2 hours at room temperature. The 1800 bp band containing the promoter/neomycin/polyA sequences was excised from the gel and extracted from the agarose using the

Wizard DNA clean up system. This fragment was ligated to the human APP cDNA-adapter generated through the follow process.

Generation of human APP cDNA's with either the Swedish-FAD, London-FAD, Swedish/London-FAD, or Swedish-FAD, APP713 mutations fused with human APP genomic sequences containing APP polyadenylation signals: Plasmid pMTI-2385-Swedish (not shown) possesses the entire human APP 695 cDNA fused with human APP cloned into pBluescript II SK+. The plasmid pMTI 2398 was derived from pMTI2385. The strategy for its creation involved the extensive use of a cDNA-genomic hybrid plasmid, pMTI2339. pMTI2385-Swedish was assembled in a four-part ligation with the following components; an ~1861 bps. XmaI-BglII fragment from pMTI2339, a ~2008 bps. SpeI-SalI fragment from pMTI2339, a ~589 bps. fragment from FAD clone #5 (contains Swedish-FAD mutation) generated by Dr. Gerhard Konig, and a pBSSK(+)II vector opened up with XmaI and SalI. The ligation was done according to standard protocols with the insert fragments being in equal molar ratios and there being a 3:1 ratio of total insert to vector. Ligation mixtures were transformed in XL-1 Blue competent cells (Stratagene) and mini-preps analyzed by an initial digestion of XmaI-SalI. Two putative clones were further characterized with BglII-SpeI, XmaI-BglII, SpeI-SalI, EcoRI, HincII, and PvuII. Two clones, #4 and #5 gave the expected results. These were grown up and sequenced confirmed.

Plasmid pMTI-2453 was derived from pMTI-2385-London. pMTI-2385-London was assembled in a four-part ligation with the following components: a ~1.7 Kb Xma I-SacI fragment from pMTI2385-Swedish, a ~350 bp SacI-StyI fragment from pMTI-104 (contains London-FAD mutation; obtained from Paul Fracasso), a ~2.5 Kb StyI-SalI fragment from pMTI2385-Swedish, and a ~2.7 kb SalI-XmaI fragment from pMTI2385-Swedish.

Plasmid pMTI-2454 was derived from pMTI-2385-Swedish/London. Swedish/London was assembled in a four-part ligation with the following components: a ~1.9 Kb XmaI-EcoRI fragment from pMTI2385-Swedish, a ~700 bp EcoRI-ClaI fragment from pMTI-2385-London, a ~1.9 Kb ClaI-SalI fragment from pMTI2385-Swedish, and a~2.7 Kb SalI-XmaI fragment from pMTI2385-Swedish.

Plasmid pMTI-2455 was derived from pMTI-2385-Swedish APP713. pMTI-2385-Swedish APP713 was assembled in multi-step process using PCR mutagenesis to introduce the APP713 stop mutation into proximity with the Swedish-FAD mutation. First, a ~560 bp EcoRI-SpeI fragment from pMTI2385-Swedish was ligated with the 2.9 Kb EcoRI-SpeI fragment from Bluescript KS+II (Stratagene) to generate pMTI-X. A ~400 bp fragment containing the APP 713 stop mutation was generated by PCR using APP cDNA as template and oligonucleotides RA39 (CCATCGATGGATCAGTTACGGAAACGATGCTCTCATGC) and RA40 (CCATCGATGGCCAAGGTGATGACGATCACTGTGGATCCCTACGCT ATGACAACACCGC) (Figure 9). The ~400 bp PCR fragment was digested with ClaI and StyI and ligated into the ~3.3 Kb ClaI-StyI fragment from pMTI-X to generate pMTI-Y. pMTI-2385-Swedish APP713 was assembled in a four-part ligation with the following components: a ~560 bp EcoRI-SpeI fragment from pMTI-Y, a ~1.9 Kb XmaI-EcoRI fragment from pMTI2385-Swedish, a ~2 Kb Kb SpeI-SalI fragment from pMTI2339, and a ~2.8 Kb fragment from Bluescript SK+II.

Generation of the human APP "Swedish" FAD mutation cDNA-neomycin sequences to fuse to the mouse APP exon 16 DNA: Four μg of plasmid pMTI-2385B was digested with 20 units of restriction enzyme SalI (cat#138L) in its ideal buffer for 2 hours at 37°C. The reaction was run through an 0.8% agarose gel in 0.5X TAE buffer at 120 volts for 1.5 hours at

room temperature. The linearized DNA band was excised and isolated away from the agarose using the Qiaex DNA Gel Extraction kit and the protocol provided (Qiagen Cat#20021). One μg of SalI-linearized p2385B was ligated to 45 pmol of annealed SalI-AflII-EcoRV-NcoI-MluI adapter (mentioned previously) in a standard ligation reaction. One-tenth of the ligation reaction was used to transform E.coli XL-1 blue cells. This p2385B-adaptor construct, 18 μg, was linearized with 60 units of EcoRV in a standard digestion reaction. Into this was added 15 units of calf intestine alkaline phosphatase and incubated at 37°C for 1 hour to dephosphorylate the 5' ends of the DNA. The reaction was stopped with EDTA at a final concentration of 5 mM and heat inactivated at 75°C for 10 minutes. The dephosphorylated plasmid was gel isolated and 1 μg was ligated to 400 ng of the 1800 bp neomycin fragment with EcoRV 5' and StuI 3' ends (mentioned in the section "Generation of cloning sites around the neomycin resistance gene"). One-tenth of the ligation reaction was used to transform E. coli XL-1 blue cells following the protocol provided by the supplier. Correct orientation constructs had the neomycin fragment (5' EcoRV site) placed immediately downstream of the human APP cDNA polyA sequences (3' EcoRV site), this construct was designated p2397+A (not shown).

Construction of the completed targeting vector containing the human APP "Swedish" FAD mutation: The 5 Kb mouse APP exon 16 containing DNA, p2396 (12 μg), was digested with 50 units of BglII in buffer 3 for 3 hours at 37°C. To 6 μg of the digest was added 10 units of CIP and incubated at 37°C for 1 hour. The reaction was stopped as mentioned above and the DNA was gel isolated using Gelase (Epicentre cat#G09100) and following the supplied protocol. The 4.5 Kb BglII fragment containing the human APP cDNA-neomycin fusion was released from p2397+A by digesting 12 μg of DNA with 28 units of NruI (cat#192L) in its ideal buffer at

37°C for 3 hours. After being confirmed of its linearization 50 units of BglII were added for an additional 2-hour incubation at 37°C. The 4.5 Kb fragment was gel isolated using Gelase and then ligated (300 ng) to the dephosphorylated p2396-BglII linearized DNA (100 ng) in a standard ligation reaction and subsequently transformed into E.coli XL-1 blue cells. The resulting plasmid with the mouse APP exon 16 fused to the human APP cDNA at exon 16 (BglII site) was designated as p2398 (Figure 5 and Figure 18).

E.2.7 Cloning of the HSV thimidine kinase (TK) gene into the targeting vector: The HSV thimidine kinase gene (from pAD7) was provided by Ann Davis. Unique restriction sites had to be engineered with the TK gene to provide linearizing access in the completed targeting vector. A 3Kb BamHI-ClaI fragment containing the murine phosphoglycerate kinase (PGK) promoter regulating the TK gene with the BGH polyadenylation sequences was isolated away from vector sequences and sub-cloned into pBluescript II SK+ at its respective sites. Twenty μg of this new TK plasmid, pCB11, was digested with 60 units of SalI in its unique buffer and incubated overnight at 37°C. The enzyme was heat inactivated at 65°C for 20 minutes and then 10 units of CIP was added for 1 hour at 37°C. The phosphatase was heat inactivated at 75°C for 10 minutes. The linearized DNA band was excised and isolated away from the agarose using the Qiaex DNA Gel Extraction kit and the protocol provided as stated above. In a standard ligation reaction, 45 ng of SalI-linearized vector was added to 15 pmol of annealed SalI-AscI-PmeI-NotI-AscI-PmeI-SalI adapter (5'TCGACAAGGCGCGCCGTTTAAACAAGCGGCCGCTTGGCGCGCCT TTTGTTTAAACTTG3') and incubated overnight at 14°C. This TK plasmid containing the restriction sites PmeI and AscI was designated as pXII28N. Five μg of pXII28N was digested with 20 units of NotI (cat#189L) and 15 units of PvuI (cat#150L) in NotI buffer (NEB) and 0.1 mg/ml BSA at 37°C

for overnight. The 3Kb NotI TK band was excised and isolated away from the agarose using the Qiaex DNA Gel Extraction kit and the protocol provided. Five hundred ng of this TK fragment was ligated to 50 ng of NotI linearized p2398 (vector containing the APP/neo sequences fused to the mouse APP exon 16 sequences) in a standard ligation reaction and incubated overnight at 14°C. The resulting targeting vector, p2399 (350 μg), was linearized with 320 units of PmeI (cat#560L) in buffer 4 (NEB) and 0.1 mg/ml BSA and incubated overnight at 37°C. Protein was removed by adding sodium acetate pH 5.2 to 0.3 M and extracting twice with Tris-Cl buffered phenol and extracting once with chloroform and ethanol precipitating at -20°C for overnight.

Construction of the completed targeting vectors containing the human APP London-FAD, Swedish/London-FAD, and "Swedish-FAD APP713 mutation: These three targeting vectors were constructed by ligating four separate fragments with one of these fragments containing one of the FAD mutations. The seminal targeting vector construct, p2398, was digested in three independent reactions to obtain three of the specific fragments. (1.) Five μg of p2398 were digested with 15 units of AflII (cat #520S) in buffer 2 with 0.1 mg/ml BSA at 37°C for overnight. To this reaction was added enough buffer 3 to adjust the concentration to 100 mM NaCl and 30 units of NotI and incubated at 37°C for 3 hours. (2.) Twenty μg of p2398 were digested with 24 units of BglII, 20 units of NotI, and 0.1 mg/ml BSA in buffer 3 at 37°C for overnight. (3.) Twenty μg of p2398 were digested with 20 units of AflII, 10 units of ClaI (cat#197L), and 0.1 mg/ml BSA in buffer 4 at 37°C for overnight. All three digestion reactions were run on 0.8% low melt agarose gels in 0.5X TAE buffer at 70 volts for 3 hours. From digestion reaction (1.) an 8Kb fragment containing the neomycin-murine APP intron 16-pBluescript sequences was excised, from reaction (2.) a 2Kb

fragment containing murine APP intron 15-exon 16 sequences was excised, from reaction (3.) a 2Kb fragment containing human cDNA/polyA sequences was excised and all the fragments were isolated away from the agarose using the Qiaex Gel Extraction kit. The last fragments to isolate were the three 700bp human APP FAD containing fragments. Twenty-five μg of each of the pMTI-2385 London (not shown), pMTI-2385 Swedish/London (not shown), and pMTI-2385 Swedish-FAD 713 (not shown), vectors were digested with 24 units of BglII, 15 units of ClaI, and 0.1 mg/ml BSA in buffer 4 at 37°C for overnight. The 700 bp bands from these digestions were isolated away from the agarose using the identical protocol as above. A four-part standard ligation reaction was combined using 25 ng of the 8 Kb AflII/NotI fragment, 250 ng of the 2 Kb AflII/ClaI fragment, 300 ng of the 700 bp BglII/ClaI fragment, and 250 ng of the 2 Kb NotI/BglII fragment and incubated at 14°C for 24 hours. One-sixth of the ligation reaction was used to transform E.coli XL-1 blue cells in a standard protocol. The resulting constructs were designated as p2450 (London-FAD), p2451 (Swedish/London-FAD), and p2452 (Swedish-FAD APP713)(not shown). The final step for each individual plasmid was to clone the TK gene fragment with NotI ends into it. Five μg of each plasmid, p2450, p2451, p2452 were digested with 20 units of NotI in buffer 3 at 37°C for 3 hours. To dephosphorylate the vector, 10 units of CIP were added to the digestion reaction and incubated at 37°C for 1 hour. The phosphatase was heat inactivated at 75°C for 10 minutes. The linearized DNA band was excised and isolated away from the agarose using the Qiaex DNA Gel Extraction kit and the protocol provided as stated above. Fifty ng of each dephosphorylated vector was ligated to 300 ng of the 3 Kb NotI TK gene fragment in a standard ligation reaction. The resulting plasmids were designated as p2453 (London-FAD; Figure 6: Figure 19), p2454 (Swedish/London-FAD; Figure 7; Figure 20), and p2455 (Swedish-FAD APP713; Figure 8: Figure 21). Each of these three targeting vectors

(500 μg) were linearized with 500 units of AscI in buffer 4 at 37°C for overnight. The DNAs were cleaned away from the enzymes by phenol/chloroform extractions as stated in the section "Cloning of the HSV thimidine kinase (TK) gene into the targeting vector". Linearized plasmids were electroporated into ES cells.

miniSouthern-blot analyses

DNA sample preparation: Potential clones were grown in a 96 well plate format. Samples were lysed with the addition of 50 μl of Lysis Buffer [10 mM Tris pH 7.5, 10 mM EDTA pH 8.0, 10 mM NaCl, 0.5% Sarcosyl, and 1 mg/ml Proteinase K (added fresh)] per well and incubated overnight at 65°C in a humidified chamber. The DNA is precipitated by the addition of 100 μl of 75 mM NaCl in ethanol followed by incubation at room temperature for 15-30 minutes. The DNA is then washed 3x with 150 μl of 70% ethanol added drop by drop to each well. After the final wash, the plate is inverted and allowed to air-dry for 5 - 10 minutes. While the plate is drying, the Restriction Enzyme Cocktail (1x Restriction Buffer specified for the enzyme being used, 1 mM Spermidine, 100 μg/ml Bovine Serum Albumin, and 10 - 20 units of enzyme) is prepared. 30 μl of this cocktail is then added to each well. Incubate overnight at the restriction enzyme's required temperature in a humidified chamber. The next day add 4-5 ml of loading dye (10 mM Tris-HCl pH 6.0, 0.25% bromophenol blue, 0.25% xylene cyanol FF, 15% Ficoll (Type 400; Pharmacia) in water, and 30 mM EDTA.) and store at -20°C.

Agarose Gel Electrophoresis: A large gel tray (Owl Scientific) is prepared with three 36-teeth combs (evenly distributed along the length of the tray) and 400 ml of molten agarose (FMC). This size of gel will accommodate one 96-well mini-Southern digest plate. The samples were

electrophoresed for approximately three hours at 120 V. After the electrophoresis was complete, the gel was denatured in 0.25 M HCl (2 x 7 minutes at room temperature) and then equilibrated in 0.4 N NaOH (1 x 20 minutes at room temperature). An overnight alkaline capillary transfer is set up in 0.4 N NaOH with Gene Screen Plus (DuPont NEN). The next day the membrane was neutralized in 2x SSC for 5-10 minutes and then UV cross-linked (Stratagene). The membrane is then stored dry until hybridization. Prehybridization was carried out in 1 M NaCl (Gibco BRL), 10% Dextran Sulphate (Pharmacia), 1% SDS (Gibco BRL), and 200 μg/ml salmon sperm DNA(Stratagene) for at least one hour at 65°C in a Robbins Hybridization Oven. The probe of interest was then labeled according to the standard protocol contained in the Prime-It II random prime kit (Stratagene). The specific activity of the probe was approximately 1 x 109 dpm/μg. It was then added directly to the prehybridization mixture at a concentration ~1 x 106 dpm/ml. The filter(s) were then hybridized for 16 hours at 65°C in the hybridization oven. The initial post - hybridization wash was carried out for 5-10 minutes at room temperature in 2x SSC (3 M NaCl, 0.3 M Sodium Citrate Dihydrate), 1% SDS. A stringent wash was then performed in 1x SSC, 0.1% SDS at 65°C for 30 minutes. The filter was then placed into a seal-a-meal bag and placed into a Fuji Phosphoimager for interpretation.

Confirmatory Southern Blots

Preparation of High Molecular Weight DNA from Cells: In order to confirm targeted clones identified in the mini - Southern paradigm, cell pellets expanded from these clones are analyzed for accurate recombination events at both the 5' and 3' ends of the targeting vector. 1 ml of Cell Lysis Buffer (100 mM NaCl, 50 mM Tris pH 7.5, 10 mM EDTA pH 8.0, and 0.5% SDS) and 20 ml of freshly prepared 40 mg/ml Proteinase K (Boehringer-Mannheim) was added to each cell pellet. The tubes were

rocked overnight at 65°C. The next day, an equal volume amount of isopropanol was added and the tube inverted several times to precipitate the DNA. The DNA was then spooled onto a flame sealed micropipette and rinsed once in 70% ethanol, once in 100% ethanol, and then air dried. The pipette was broken off into a sterile Eppendorf tube and the DNA dissolved in 200 μl of sterile TE overnight at room temperature. The DNA is then stored at 4°C until restriction enzyme analysis.

Agarose Gel Electrophoresis: Restriction enzyme digested DNA is gel analyzed as described above in the mini-Southern methods except the number and sizes of the combs vary. Denaturation, renaturation, and capillary transfer were performed as described previously. Probes of interest were also labeled in the same manner as described above. Interpretation of results were facilitated by phosphoimaging as previously described.

Gene-targeting in ES cells

Culture of ES cells: Procedures were performed essentially as describe in E. J. Roberstion (Robertson, 1987) . ES cell were propagated using Mitomycin C treated SNL76/7 STO feeder cells (cell line obtained from A. Bradley) and modified DMEM culture media (supplemented with 15% FCS,1X GPS,1X BME).

Electroporation of ES cells: DNA was linearized with the appropriate restriction enzyme then extracted with an equal volume of phenol/chloroform and once with an equal volume of chloroform and precipitated with 2.4 volumes of ethanol. The DNA was resuspended at 1 mg/ml in sterile 0.1X TE (25 ml of DNA per electroporation). Embryonic stem cells (80% confluent) were passaged 1:2 the day before electroporation. Cells to be electroporated were fed 4 hours before harvesting. The cells were trypsinized and resuspend in media (cells from 2 x 10 cm plates can be combined in a total volume of 10 ml in a 15 ml tube). The cells were pelleted and resuspend in 10 ml PBS at a density of 11 x 10^6 cells/ml. The appropriate amounts of DNA and cells were mixed together in a 15 ml tube (25 ml of DNA and 0.9 ml of cells for each electroporation) and allowed to sit at room temperature for 5 minutes. The cell/DNA mixture (0.9 ml) was transferred to electroporation cuvettes and an electrical current was passed through the solution (using Biorad GenePulser at 230V and 500 mF). The cells were then transferred to culture plates with feeder cells (up to 2 x 10^7 cells/100 mm plate or 6 x 10^6 cells/60 mm plate). After 24 hours of culture in modified DMEM the cells were cultured in DMEM selection containing G418 and 0.2 mM FIAU. Resistant colonies may be picked as early as 8 days, are best around 10-11 days, but may be recovered up to 18-21 days after the electroporation. Picked colonies are transferred to 96 well plates with feeders

cells and screened for gene-targeting events by mini-Southtern-blot analysis (see below).

Production of chimeric mice: Procedures were performed essentially as described by A. Bradley (Bradley, 1987) . Host 3.5 day blastocysts were derived from timed matings of C57BL/6 mice and cultured in M16 media. Approximately 14 targeted ES cells were injected into each blastomere. Surviving blastocysts were then surgically reimplanted (approximately 12 per animal) into pseudopregnant ICR female mice essentially as described (A. Bradley). Chimeric mice were born about 17 days after implantation.

Genotype analyses of transgenic mice

Identification of mice possessing the targeted human APP cDNA by PCR screening: When mice were older than 2 weeks of age their tails were biopsies to obtain genomic DNA for analysis. One centimeter pieces of tail were prepared using the QIAamp Tissue Kit (Qiagen cat# 29304) and following the protocol provided. Genomic DNA was eluted in 150 μl of 10 mM Tris-Cl pH 9 and used in two independent PCR assays; (1) to determine the endogenous mouse APP allele that remained intact: total reaction volume of 50 μl - 5 μl of genomic tail DNA (approximately 1 μg), 5 μl of 10X buffer 8 (Stratagene cat#200430), 5 μl of 2 mM dNTP mix, 200 ng of oligonucleotide KC125 (5'ACTTTGTGTTTGACGC3'), 200 ng of oligonucleotide KC132 (5'CAGTTTTTGATGGCGG3'), 1 unit of Perfect Match Polymerase Enhancer, 2.5 units of AmpliTaq and 100 ng each of oligonucleotides 6&7 and (2) to determine the targeted mouse APP allele: total reaction volume of 50 μl - 5 μl of genomic tail DNA (approximately 1 μg), 5 μl of 10X buffer 8 (Stratagene cat#200430), 5 μl of 2 mM dNTP mix, 200 ng of oligonucleotide KC125 (5'ACTTTGTGTTTGACGC3'), 200 ng of oligonucleotide KC131 (5'GATGATGAACTTCATATCCTG3'), 1 unit of

Perfect Match Polymerase Enhancer, 2.5 units of AmpliTaq and 100 ng each of oligonucleotides 6&7. The reactions were run in a Perkin Elmer turbo 2400 thermal cycler. The parameters of the run were as follows: one cycle at 94°C for one minute, 30 cycles at 94°C for 30 seconds-56°C for 50 seconds-70°C for two minutes, maintain at 10°C indefinitely. Oligonucleotides 6 (5'CCTCGGCCTTTGGTGTGTGTTTTATGACATGACCCCCTTGA) & 7 (5'CACCCTGTTGTCAATGCCTCTGGGTTTCCGCCAGTTTCG3') are homologous to mouse ribosomal protein L32 sequences within intron 2 and exon 3, respectively, and used as an internal DNA control signal. One-fifth of each PCR reaction was run on a 6% polyacrylamide gel (Novex cat#EC6265) in 1X TBE (89 mM Tris borate, 2 mM EDTA) buffer at 125 volts for 35 minutes and stained in 1 mg/ml EtBr for 15 minutes and photographed.

RNA analyses

RNA isolation: Total brains were dissected and flash frozen on dry ice from two negative litter mates, two heterozygous targeted mice, and two homozygous targeted mice. In addition, kidneys and tails were also removed from these mice and flash frozen. The brains were divided in half, one for the RNA analysis and the other for protein analysis. To one-half of each brain was added 5 ml RNAzolB (Tel-Test, Inc. cat#CS-105) and the tissues were homogenized using a Brinkman Polytron at medium speed for 20 seconds. Chloroform, 500 μl, was added to the homogenized tissue and shaken well for 10 seconds and incubated on ice for 15 minutes. The samples were spun in a tabletop Sorvall centrifuge at 1500Xg for 20 minutes at 4°C. The aqueous phase was removed and added to an equal volume of isopropanol, mixed, and incubated on ice for 15 minutes. The samples were spun in a Sorvall RC-5B centrifuge with an SS-34 rotor at 7500Xg at 4°C for

25 minutes. The supernatants were removed and the pellets were rinsed twice in cold 70% EtOH and air dried. The total RNA pellets were resuspended in 500 ml H_2O and incubated at 65°C for 10 minutes to more easily get the RNA into suspension. These RNA samples were used to obtain polyadenylation specific mRNA using the PolyAtract mRNA isolation system III kit (Promega Z5300). The protocol followed was provided by the supplier and yields ranged from 3 to 6 μg of mRNA.

Northern blot analyses: These samples were then used in a Northern blot to see the sizes of these targeted hybrid APP transcripts. The RNA was run on a 1.2% agarose (FMC cat# 50072) , 2.2 M formaldehyde gel prepared as follows: 0.6g agarose in 36 ml H_2O were melted in a microwave and placed at 60°C. When the gel cooled to 60°C , 5 ml of 10X MOPS (0.4 M MOPS (Sigma MESA M-5755) pH7, 0.1 M sodium acetate, 10 mM EDTA pH8) running buffer and 9 ml of 37% formaldehyde (pH >4) were added, mixed and left at 45°C until ready to pour. The RNA samples were prepared in a total volume of 30 μl - 3 μl 10X MOPS buffer, 5.25 μl 37% formaldehyde, 15 μl formamide, and 6.75 μl mRNA (0.5 μg) were mixed well and incubate at 55°C for 15 minutes. To this was added 6 ml formaldehyde loading buffer (1 mM EDTA pH8, 0.25% bromophenol blue, 0.25% xylene cyanol, 50% glycerol) and 1 ml 1 mg/ml EtBr. The samples were loaded into the gel and run at 5V/cm (55-75V) for 3hr in 1X MOPS buffer. The gel was rinsed in H_2O several times and soaked in 0.05N NaOH for 30 minutes under gentle shaking. The gel was then equilibrated twice for 15 minutes in 20X SSC and transferred by wick assembly for 16 hours in 20X SSC. The membrane used for transferring was Hybond-N+ (Amersham cat#RPN2020B) which is a 0.45 micron nylon membrane. After transfer was completed the membrane was rinsed in 2X SSC for 10 minutes and UV cross-linked in a Stratalinker mentioned earlier. The membrane was pre-hybridized

in 10 ml 0.5 M sodium phosphate pH7, 1% BSA, and 7% SDS for 4 hours at 65°C in a Robbins Hybridization Oven (model 400). This solution was removed and replaced with fresh hybridization solution and 6x107 counts of denatured APP probe and 8x105 counts of denatured mouse beta-actin probe and hybridized overnight at 65°C. The membrane was washed in 2X SSPE, 0.1% SDS at 25°C for 10 minutes, twice, and then washed in 1X SSPE, 0.1% SDS (pre-warmed) at 65°C for 15 minutes. The membrane was exposed to a phosphoimaging screen for 24 hours and developed.

Probes for Northern blot: Both the APP probe (homologous to the murine and human sequences) and the murine beta-actin probe were prepared in identical protocols. The APP DNA used to make the probe was an NruI/XhoI 900bp fragment from p2385B. The murine beta-actin 430bp DNA used for the probe came from a PCR reaction where the exon 3 of B-actin was amplified using these two oligonucleotides: KC137 (5'GTTTGAGACCTTCAACACCC3') and KC138 (5'GAAGGAAGGCTGGAAAAGAGCC3'). The probes were labeled using the Prime It II kit (Stratagene cat#300385) and following the protocol provided. After the reactions were stopped they were put over a G-50 spin column (5'-3' cat# 5303-633329) to remove the un-incorporated nucleotides.

To increase the level of APP-specific mRNA from the polyA selected RNA, the samples were annealed to an APP specific oligonucleotide (RA49-5'CGATGGGTAGTGAAGCA3')) that was homologous to both the murine and human sequences approximately 40nt 3' of the stop codon. The assay was performed using the Superscript II RT-PCR kit (Gibco/BRL cat# 18089-011). In a reaction volume of 14 μl was combined 0.1-0.15 μg polyA mRNA and 600 ng RA49 and incubated at 70°C for 10 minutes and 4°C for 10 minutes. To this was added 2 μl 10X synthesis buffer, 1 μl 10X dNTP mix, 2 μl 0.1 M DTT, and 200 units of Superscript II reverse transcriptase (all

supplied by the kit) and the incubations continued at 25°C for 10 minutes, 42°C for 50 minutes, 70°C for 15 minutes, and 4°C for 10 minutes. The reactions were then treated with 2 units of RNaseH for 20 minutes at 37°C and then placed on ice. After the RNA was removed from the cDNA the next step was the amplification reaction: 20 μl of cDNA reaction mix, 8 μl 10X synthesis buffer, 300 ng of oligonucleotide KC56 (5'GTGAAGATGGATGCAGAATTC3'), 300 ng of oligonucleotide KC56 Swedish (5'GTGAATCTAGATGCAGAATTC3'), 600 ng of oligonucleotide RA49, and 5 units of AmpliTaq in a total volume of 100 ml. The amplification was run in the Perkin Elmer turbo 2400 using the same parameters as stated in "Identification of mice possessing the targeted human APP cDNA by PCR screening". The RT-PCR reactions were subjected to restriction enzyme digestions taking advantage of the restriction site polymorphism between the murine and human APP sequences. One-tenth of the RT-PCR reaction was digested with 30 units of SalI and 0.1 mg/ml BSA in its ideal buffer at 37°C for 2 hours, another set was digested with 30 units of StyI in buffer 3 at 37°C for 2 hours. The digests were run out on a 4% polyacrylamide gel in 1X TBE at 150 volts for 1 hour and stained in 1 mg/ml EtBr for 15 minutes and photographed. All oligos were provided by Midland and all restriction enzymes by NEB.

Protein Analysis

Tissue Extraction: This protocol is generally used for mouse tissue with no more than several hundred mgs of tissue available, therefore all volumes must be kept to a minimum. Tissue was homogenized in 1 ml of RAB buffer (0.1 M MES pH 7.0, 0.75 M NaCl, 0.5 M $MgCl_2$, 1 mM EGTA, 1 mM DTT) containing proteinase inhibitors. The protease inhibitor cocktail contains 1x Aprotonin (0.41 trypsin inhibitor units/mg protein), 1x PMSF (2 mM in isopropanol), 1x Protease inhibitor mix (chymostatin,

leupeptin, antipain, and pepstatin) each at 50 μg/ml in DMSO, and 1 mM EDTA. A 7 ml dounce tissue grinder (Wheaton) was used for homogenization. The tissue homogenate was spun at 40K in the Beckman TL100 using the fixed angle rotor for one hour. The supernatant from this spin was saved as it contains the soluble APP. The pellet was homogenized in 1 ml of RAB plus protease inhibitors and 30% sucrose (Sigma). Spin for one hour at 40K in the Beckman TL100. This serves as a wash and demylelinating step. Discard the supernatant from this spin and homogenize the pellet in 1 ml of RIPA buffer (150 mM NaCl, 1% NP-40, 0.5% deoxycholate (Na salt), 0.1% SDS, and 50 mM Tris-Cl pH 8.0). This should contain the membrane associated form of APP. The amount of protein can then be quantitated by using the BCA Protein Assay Reagent Kit (Pierce). This quantitation allows equal amounts of total protein to be loaded on polyacrylamide gels and direct comparisons of transgenic and non-transgenic expression patterns and levels to be made.

Immunoprecipation: The final adjusted volume of the immunoprecipitation was 1 ml in RIPA buffer. The amounts of antigen and antibody to add varied from experiment to experiment depending on the concentrations of both. Antibody and antigen were incubated for two hours at 4°C while gently spinning on a rotating wheel. 50 μl of goat anti-mouse or anti-rabbit IgG bound to agarose (Sigma) was added to the antigen/antibody and incubated for another two hours at 4°C on the rotating wheel. Agarose IgG-antigen/antibody complex was rinsed by pelleting at 12,000 x g for 1 min. and then removing the supernatant. Then 500 μl of ice cold RIPA buffer was added to the pellet, resuspended, and incubated for 10 minutes on ice. The samples were then spun at 4°C. The rinses were repeated twice more, but the 10 minute incubation step was omitted. To the rinsed pellet, was added 50 μl of 1x sample buffer (Novex)plus 2 ml of beta-

mercaptoethanol (Aldrich). Samples were boiled for 10 minutes and spun for 1 minute at room temperature. The supernatant was transfered to a fresh tube and store at -20°C.

Western Blotting: Polyacrylamide gel electrophoresis (PAGE) and electroblottting were accomplished utilizing the X-Cell II Gel and Blot Module (Novex) and pre-casted polyacrylamide gels (Novex). The selection of a particular separation scheme depended on what form of the Alzheimer Precursor Protein (APP) was being examined. For C-terminal fragments 16% Tris-Tricine gels were utilized, holo APP utilized 10-20% Tris-Tricine gels, and to elucidate form differences (Kunitz vs. 695) of the holo-APP, 6% Tris-Glycine gels were used. Samples prepared as described above were loaded onto gels and electrophoresed at 120V for approximately 90 minutes. The gels were then transferred to nitrocellulose membranes (Novex) for 1-2 hours at 30V. Non-specific sites were then blocked by incubation of the filter in 5% non-fat dry milk (NFDM) for 1 hour at room temperature while gently rocking. Primary antibody was then added at a dilution of 1:500 in 5-10 ml of NFDM, added to the membrane and sealed in a seal-a-meal bag. This was incubated overnight at room temperature while gently rocking. The membrane was then rinsed for 1 hour at room temperature with several changes of 5% NFDM. A ^{35}S labeled secondary antibody (Amersham), either anti-mouse IgG or anti-goat IgG, was then added and incubated for 1 hour at room temperature while gently shaking. The membrane was then rinsed for 15-30 minutes in 5% NFDM and then equilibrated into 1x phosphate buffered saline (PBS, Gibco BRL) for 15 minutes. The filter was then dried and either placed on a phosphoimaging plate or with a piece of X-OMAT X-ray film (Kodak).

APP Antibodies: Monoclonal antibody (MAb) 4G8 (Senetek) was used for the immunoprecipitation of APP holoprotein and C-terminal fragments at a dilution of 1:100 (~10-20 μg/ml). MAb 286.8 (BRC) was used for the immunoprecipitation of APP holoprotein at a dilution of 1:100 (~10-20 μg/ml). MAb 6E10 (Senetek) was used as a detection reagent on Western blots at dilutions of 1:500. Polyclonal antibody (PAb) 369 (generously provided by Dr. Sam Gandy) was used for both the immunoprecipitation of APP holo-protein (1:100) and for a detection reagent for C-terminal fragments (1:500). MAb 22C11 (generously provided by Dr. Konrad Beyreuther) was used as a detection agent for APP holo-protein at a dilution of 1:500.

FAD-m/hAPP gene products expressed in transgenic mouse lines

Transgenic mouse lines ES5007, ES5103, ES5401, and ES5403 were generated by mutating the mouse APP gene via homologous recombination in embryonic stem (ES) cells (see below). The gene products expressed in the transgenic mouse lines are described schematically in Figure 10. m/hAPP770 represents the largest (770 amino acid residues) of the various alternative splice forms of protein expressed by each mutated mouse APP gene. m/hAPP exhibits amino acid sequence identity with mouse APP with the exception of those residues indicated by (asterisks, *). In all cases the beta-amyloid (bA4) domain (Asp672 to Thr714; 43 amino acid residues) has been "humanized" by the introduction of three amino acid substitutions (as indicated by green asterisks); Gly(676) to Arg, Phe(681) to Thr, and Arg(684) to His. Transgenic mouse line ES5007 also has the Swedish-FAD mutation [Lys,Met(670,671) to Asn,Leu] introduced into the mouse gene. Transgenic mouse lines ES5401 and ES5403 have the London-FAD mutation [Val(717) to Ilu] and transgenic line ES5103 carries both Swedish and London FAD mutations. In addition to the Swedish FAD and "human"

mutations, a transgenic mouse line ES5215 can also be produced which has a premature stop codon introduced at position 714.

Gene-Targeting Vectors

The targeting vectors were designed in such a way as to facilitate the integration of human cDNA sequences into mouse exon 16. The targeting constructs function as replacement-type vectors with both positive (neomycin resistance gene) and negative (HSV TK gene) selection genes (figure 11). To facilitate homologous recombination, a mouse genomic clone encompassing exon 16 was obtained by screening a mouse genomic lambda library. A lambda clone, "35A", was identified which contained an intact exon 16 (figure 1). Nco I fragments of mouse genomic clone 35A were subcloned into the BSII SK+ vector and the subclones (pRA3, pMTI-2396, and pN2C4) were characterized by DNA sequence and restriction enzyme analyses (see Figures 2, 3, and 4). The 5.5 Kb Nco I DNA fragment (subcloned into pMTI-2396) contains APP exon 16 and ~1.9 Kb and ~3.5 Kb from introns 15 and 16 respectively (Figure 2). The Nco I DNA fragment, containing exon 16, was the template upon which the gene-targeting vectors were constructed.

The gene-targeting vectors were designed so that mouse exon 16 gene sequences were fused (at a common Bgl II site) with human cDNA sequences which encode the remainder of exon 16 and exons 17 and 18 (figure 11). The mouse and human cDNA sequences encode the identical protein sequence with the exception of 3 amino acid differences (shown as green asterisks) which reside within the beta-amyloid domain. The mouse genomic-human cDNA fusion effectively "humanized" the beta-amyloid domain and facilitated the introduction of specific FAD mutations while leaving the remainder of mouse APP protein sequences unchanged (see Fig 13).

The human cDNA was mutagenized to encode either the "Swedish"-FAD, "London"-FAD , "Swedish"/"London"-FAD (shown here), or "Swedish"-FAD APP713 mutations (shown as black asterisks) of APP (see Fig. 10 and Table I). The mutagenesis of the "Swedish"-FAD mutation also incorporated a new Xba I restriction site. Proper RNA processing was ensured by fusing the 3'-end of the human cDNA sequence with human genomic sequences which contain transcription termination and poly-adenylation signals from the human APP gene. A neomycin gene was inserted in-between the 3'-end of the human APP polyadenylation signal and mouse APP intron 16 sequences. Targeting vector pMTI-2398 (Swedish-FAD) contained the neomycin resistance gene and not the HSV TK gene. This vector was linearized with Pme I and was used to generate transgenic mouse line ES5007. (Tables I and II).

For the remaining three targeting vectors, a HSV Tk gene was inserted into the clone in such a way that its placement was outside of the genomic domains homologous to mouse (Figure 11; as shown or in the opposite orientation; the orientation was not critical). Targeting vector pMTI-5453 encodes London-FAD m/hAPP, targeting vector pMTI5454 encodes Swedish/London-FAD m/hAPP, and targeting vector pMTI-5455 encodes Swedish-FAD m/hAPP713. These targeting vectors were linearized with Asc I and were used to generate transgenic lines. (Tables I and II).

Gene-targeting in embryonic stem (ES) cells

The targeting vectors were designed to function as replacement-type vectors with both positive (neomycin resistance gene) and negative (HSV TK gene) selection genes. After electroporation of the targeting vector into ES cells, G418 drug treatment selected for ES cells which had integrated the targeting vector (including the neomycin resistance gene) into the mouse genome. The majority of G418 resistant ES cell clones had targeting vector

integrated at random locations of the genome. These ES cell clones retained an intact HSV TK gene and were not desired. The clones containing random integrations could be eliminated by treatment with FIAU selection media which is toxic only to cells expressing HSV TK. If, as desired, the mouse APP gene is targeted via a double-crossover homologous recombination event, the flanking non-homologous HSV TK DNA sequences are lost (as shown in fig 12) and the ES cells are resistant to FIAU treatment.

Homologous recombination between mouse APP exon 16 locus and the gene-targeting vector fundamentally alters the manner by which the gene encodes APP (see figure 13). Normally, the beta-amyloid, transmembrane, and cytoplasmic domains of mouse APP are encoded by three separate exons. In addition, the coding region for the beta-amyloid domain resides both on exons 16 and 17. After homologous recombination with the gene targeting vector, however, mouse exon 16 gene sequences are fused with human cDNA sequences. Mouse exons 17 and 18 are now displaced down-stream from the neomycin resistance gene and are inactive. The human cDNA now functions in place of mouse exons 16, 17, and 18 to encode APP. Therefore, the beta-amyloid, transmembrane, and cytoplasmic domains of mouse APP are now encoded by human cDNA sequences.

The gene products of this new mouse genomic-human cDNA fusion are designated m/hAPP. Human cDNA sequences (exons16, 17, and 18) encode the identical protein sequence with the exception of 3 amino acid differences (shown as green asterisks) which reside within the beta-amyloid domain. The mouse genomic-human cDNA fusion effectively "humanizes" the beta-amyloid domain and facilitates the introduction of specific FAD mutations (shown as black asterisks) while leaving the remainder of mouse APP protein sequences unchanged. The human cDNA has been mutagenized to encode either the "Swedish"-FAD, "London"-FAD , "Swedish"/"London"-

FAD (shown in figure 2c), or "Swedish"-FAD APP713 mutations of APP (see also Fig. 10 and Table I).

Identification of targeted ES cell clones

After electroporation of each targeting vector (see Table I), ES cells were cultured for approximately 2 weeks in the presence of both positive (G418) and negative (FIAU) selection compounds. Four hundred G418/FIAU resistant ES cell colonies (clones) were then individually picked and cultured separately in 96 well culture dishes. The culture dishes were replica-plated, one set of copies was frozen to maintain the clones and the other replicate set was utilized for genetic analyses. From each well, DNA was extracted, digested with restriction enzyme, and analyzed by miniSouthern-blot analyses (see below). ES cell clones which appear to contain a targeted APP gene locus were thawed and expanded in culture. Gene-targeting was confirmed by Southern-blot analyses using DNA extracted from these expanded clones prior to introduction of the ES cell into the mouse germline (see below).

The mutagenesis of human cDNA's to encode the Swedish-FAD mutation also created a new Xba I (shown as X) restriction enzyme site (Figure 14). Incorporation of human FAD cDNA (shown in red) into the targeted m/hAPP gene locus thus changes the pattern of DNA fragments generated after digestion of this locus with Xba I. Using Southern-blot analyses, ES cell clones having the targeted m/hAPP gene can be distinguished from neomycin resistant ES cell clones having undesired random integrations of the targeting vector. The mouse exon 16 gene locus can be detected using a 3Kb Nco I (N) DNA fragment from intron 15 of the mouse APP gene as probe. Digestion of the mouse APP gene with Xba I generates an approximately 9 Kb DNA fragment whereas Xba I digestion of the targeted Swedish-FAD m/hAPP gene gives an approximately 5 Kb DNA

fragment when detected by Southern-blot analysis (see figure 14). This detection strategy applies to the Swedish-FAD m/hAPP, Swedish/London-FAD m/hAPP, and Swedish-FAD APP713 mutations.

Mini-Southern blot analysis identified 4 ES cell clones which appeared to contain the targeted Swedish-FAD m/h APP locus (data not shown). These clones were expanded and subsequent Southern-blot analysis demonstrated that ES cell clones A79, A80, and B12 contain the Swedish FAD APP mutation while clone A72 did not (Figure 15). DNA extracted from ES cell pellets was examined by Southern-blot analysis using the restriction enzyme Xba I as described in Figure 14. A single ~9Kb DNA fragment is observed in non-targeted ES cells whereas targeted ES cell clones exhibit both the non-targeted allele (~9Kb fragment) and the FAD mutant allele giving rise to a ~5 Kb band. Transgenic mouse line ES5007 was derived from ES cell clone B12 (Table I). The remaining positive ES cell clones failed to establish germline transmission of the FAD mutation.

Initial miniSouthern-blot analyses identified five ES cell clones which appeared to contain Swedish/London FAD APP double mutation (data not shown). DNA extracted from pellets of expanded ES cell clones was examined by Southern-blot analysis using the restriction enzyme Xba I as described in Figure 14. This analysis confirmed that ES cell clones C82, C87, D25 and D92 contained the Swedish/London FAD m/hAPP double mutation while clones C52 and D49 did not. Transgenic mouse line ES5103 was derived from ES cell clone C87 (see Table I). The remaining positive ES cell clones failed to establish germline transmission of the FAD mutation. Confirmatory Southern-blot analyses identified multiple clones which carry the Swedish-FAD m/hAPP713 mutations (data not shown).

While identical in all other respects, the targeting vector encoding London-FAD m/hAPP does not carry the Xba I restriction site associated with the Swedish mutation. It was necessary, therefore, to identify restriction

enzymes which could distinguish between un-altered ES clones and those ES cell clones containing a targeted m/hAPP allele. The restriction enzymes Bcl I and BpM I were found to distinguish between DNA from a non-targeted ES cell clone (clone A1) and DNA from clone A21 which contains the Swedish-FAD m/hAPP gene locus (data not shown, see also figure 19). Bcl I and BpM I can be used to identify targeted clones derived from any of the aforementioned gene-targeting vectors.

Using restriction enzyme Bcl I, miniSouthern-blot analysis identified 6 ES cell clones which appeared to contain the London-FAD mutation (data not shown). Confirmatory Southern-blot analysis , using restriction enzyme BpM I, demonstrated that ES cell clones D12, D60, D70, D74, and D90 contained the London-FAD m/hAPP targeted locus while clone D45 did not (figure 18). After digestion with BpM I, three DNA fragments (~6 Kb, ~3.8 Kb, and ~2.2 Kb) are observed in non-targeted ES cells whereas targeted ES cell clones exhibited an additional ~4.8 Kb DNA fragment from the targeted allele (see A21 targeted for Swedish mutation. Transgenic mouse lines ES5401 and ES5403 were derived from ES cell clones D12 and D60 respectively (Table I). The remaining positive ES cell clones failed to establish germline transmission of the FAD mutation.

Germline-transmission of targeted m/hAPP genes

ES cells, confirmed to contain a targeted m/hAPP allele, were injected into the blastocoel cavity of a 3.5 day pre-implantation embryo (blastocyst). The injected blastocysts were then surgically reimplanted into pseudopregnant fosters and chimeras were born after approximately 17 days. The ES cells were derived from the 129SVEV inbred mouse strain which has a dominant agouti coat color gene. The blastocysts were derived from the C57BL/6 inbred mouse strain which carries a recessive black coat color gene. The coat color of chimeric mice whose cells are predominately derived from the ES

cells (designated as "high percentage chimeras") is mostly agouti with small patches of black. To establish germline transmission of the targeted APP gene, high percentage chimeric male mice were mated with either 129/SVEV inbreed or black Swiss outbreed females. The genotype of offspring from ES5007, ES5103, ES5401 and ES5403 breeding pairs was determined by either Southern-blot or PCR analyses.

The Southtern-blot analyses could distinguish between non-targeted, heterozygous, and homozygous progeny mice. The analyses utilized either Bcl I or BpM I restriction enzyme, and the ~3.0Kb intron 15 DNA fragment as probe (see Figure 14 for description of probe). A Southern-blot characterizing DNA from progeny of heterozygous ES5007 breeding pairs was performed. The technique can be applied to all the aforementioned transgenic lines. Bcl I digestion of non-transgenic (wt) mouse DNA and non-targeted ES cell DNA generated ~16 and ~8.5 Kb DNA fragments. However, Bcl I digestion of heterozygous transgenic mouse DNA and targeted ES cell DNA generated ~16 , ~8.5, and ~8.0 Kb DNA fragments. Digestion of homozygous mouse DNA with Bcl I liberated ~8.5 and ~8.0 Kb DNA fragments. BpM I digestion of non-transgenic (wt) mouse DNA and non-targeted ES cell DNA generated ~6.0, ~3.8, and ~2.2 Kb DNA fragments. Bpm I digestion of heterozygous transgenic mouse DNA and targeted ES cell DNA generated ~6.0 , ~4.8, ~3.8, and ~2.2 Kb DNA fragments Digestion of homozygous mouse DNA with BpM I liberated ~6.0 , ~4.8, and ~2.2Kb DNA fragments.

The genotype of offspring from ES5007, ES5103, ES5401 and ES5403 breeding pairs was also determined by PCR analyses using a combination of oligo pairs specific to human APP (H) and mouse APP (M) sequences. Like the Southern-blot technique, PCR analysis can distinguish between non-targeted, heterozygous, and homozygous progeny mice. As an internal standard, a 154 bp region of the mouse ribosomal subunit L32 gene is

amplified using the PCR oligo pair 6 and 7 (Figure 9). This control reaction was performed in each reaction. A 118 bp region specific to the mouse APP gene is amplified using the "M" oligo pair (oligos KC125 and KC132; Figure 9) and a 109 bp region specific to targeted m/hAPP gene in amplified using the "H" oligo pair (oligos KC125 and KC131; Figure 9). A PCR reaction using non-transgenic mouse DNA (wt) gives rise to a 118 bp fragment using the "M" oligo pair but no reaction product using the "H" oligo pair. Conversely, a PCR reaction using DNA from transgenic mice homozygous (homoz.) for the targeted m/hAPP gene gives rise to a 109 bp fragment using the "H" oligo pair but no reaction product is observed using the "M" oligo pair. A PCR reaction using DNA from heterozygous transgenic mice (heter.) gives rise to both mouse and human PCR reaction products.

Messenger RNA (mRNA) expression in transgenic mouse brain

Analysis of APP mRNA composition in control mouse and ES5007 mouse brain has been determined using both Northern-blot and rtPCR analyses. RNA analyses have yet to be performed on the ES5103, ES5401, and ES5403 lines (Table II).

APP mRNA transcripts from control and ES5007 mouse brain were detected by Northern-blot analysis using an approximately 900 bp Nru I- Xho I fragment from pMTI-2385B (human APP cDNA) as probe. Mouse beta-actin mRNA was detected using a 430 bp mouse beta-actin cDNA probe (430 bp PCR product generated using oligos KC137 and KC138; see Figure 9) and served as an internal standard. mRNA from human brain (Clonetech) served as a positive control.

mRNA from the Swedish-FAD m/hAPP gene was abundantly expressed in the brain from homozygous ES5007 mice. The amount of Swedish-FAD m/hAPP mRNA in ES5007 brain was determined by phosphoimage analysis and shown to be approximately 55% of the mAPP

mRNA levels observed in control mouse brain. In concordance, the APP mRNA levels in heterozygous ES5007 mouse brain were found be approximately 75% of the level observed in control mouse brain.

The reverse transcriptase-PCR (rtPCR) technique was used to identify mouse APP and m/hAPP transcripts in mouse brain. Homozygous ES5007 mice were found to express mRNA exclusively from the targeted Swedish-FAD m/hAPP gene. No mRNA species containing sequences from mouse APP exons 16, 17, or 18 was detected in homozygotes. Heterozygous ES5007 mice were found to express mRNA transcripts from both mouse APP and Swedish-FAD m/hAPP alleles.

mRNA was purified from control and transgenic mouse brain and cDNAs were prepared using reverse transcriptase and oligonucleotide RA49 as primer. A 367 bp DNA fragment was amplified from mouse APP and m/hAPP cDNA by PCR using oligonucleotides KC56 and RA49 (Figure 9). Oligonucleotides KC56 and RA49 exhibit sequence identity with both mouse and human sequences. The mouse and human sequences were distinguished from each other by the presence of a Sty I restriction site in the human cDNA and the absence of the Sty I site in the mouse cDNA. Digestion of the 367 bp PCR product from m/hAPP cDNA generates two fragments (151 bp and 216 bp) while the PCR product from the mouse APP cDNA is not digested and remains unchanged at 367 bp.

APP mRNA from control mouse brain was amplified by rtPCR to generate a 367 bp DNA fragment that was resistant to Sty I digestion. rtPCR amplification of m/hAPP mRNA from the brain of homozygous ES5007 mice gene generated two fragments (151 bp and 216 bp) upon digestion by Sty I. No 367 bp DNA fragment remained, demonstrating that mouse APP cDNA was not present. All three DNA fragments (151 bp, 216 bp, and 367 bp) were observed after Sty I digestion of rtPCR product derived from heterozygous ES5007 brain transcripts. As a control, Sty I digestion of PCR

products from human APP cDNAs derived from human mRNA and mRNA from a HEK293 cell line expressing human APP generated the 151 and 216 bp DNA fragments. As expected, Sty I failed to digest the 367 bp PCR product derived from mouse brain mRNA.

m/hAPP protein expression in transgenic mouse brain

Swedish-FAD m/hAPP protein is expressed in the brain of ES5007 mice. MAb 286.8 specifically immunoprecipitates human APP and but not mouse APP. The epitope for MAb 286.8 has been determined to lie within the N-terminus of the human beta-amyloid domain (P. Graham et al. 1994, Pharma Report MRC 00116). The m/hAPP gene product could be specifically immunoprecipitated from a ES5007 brain homogenate using the monoclonal antibody (MAb) 286.8. APP moieties were then visualized by Western-blot analysis using MAb 22C11 as the detection antibody. MAb 22C11can detect both mouse APP and m/hAPP. Therefore, if mouse APP was present after the immunoprecipitation it would have been detected by MAb 22C11. MAb 286.8 immunoprecipitated baculovirus derived human APP but did not recognize mouse APP in mouse brain homogenates.

The immunoprecipitations were performed using equal amounts of control mouse and ES5007 brain homogenates directly applied to the Western-blot. The relative intensities of the mouse APP and m/hAPP bands were equivalent.

Baculovirus derived human APP was directly applied to the Western-blot. An equal amount of human APP was detected after immunoprecipitation by MAb 286.8. It can be concluded, therefore, that MAb286.8 efficiently immunoprecipitated human APP.

The expression of Swedish-FAD m/hAPP protein was further demonstrated by Western-blot analyses using additional detection antibodies. m/hAPP was immunoprecipitated from a homogenate of ES5007 brain using

human-specific MAb286.8. APP was then detected by Western-blot analysis using either the polyclonal antibody (PAb) 369 or MAb 6E10 for detection. MAb 6E10 is human APP specific and recognizes the human beta-amyloid domain. Again MAb 286.8 immunoprecipitates human APP, Swedish-FAD m/hAPP but does not immunoprecipitate mouse APP.

Swedish-FAD m/hAPP protein is expressed in the brain of homozygous ES5007 mice at approximately 87% of the level observed for mouse APP in non-transgenic mice. The relative expression values were determined in 3 independent Western-blot analyses using homogenates of brains from 4 homozygous ES5007 and 4 non-transgenic mice. The levels of m/hAPP protein expression ranged from 62% to 130% of control mouse APP depending on the protocol. In one experiment, APP was immunoprecipitated from equal amounts of brain homogenates from non-transgenic and homozygous ES5007 mice using PAb 369. For the other two Western-blot analyses, MAb 4G8 was used to immunoprecipitate APP. In all Western-blots, mouse APP and Swedish-FAD m/hAPP were visualized using MAb 22C11 as the detection antibody.

Processing of C-terminal domain of APP

The Swedish FAD mutation significantly altered the proteolytic processing of the of APP resulting in a change in theC-terminal fragments of APP. The observed changes in processing was consistent with a predominat usage of the beta-secretase site over the alpha-secretase site.

Membrane preparations from brain homogenates were solubilized by detergents and APP holoprotein and C-terminal fragments were immunoprecipitated using MAb 4G8. Mouse APP and m/hAPP holoproteins were detected by Western-blot analysis using MAb 22C11. The C-terminal fragments from both mouse APP and m/hAPP were detected using PAb369 while C-terminal fragments derived exclusively from m/hAPP were detected

using human specific MAb 6E10. The expression level of m/hAPP in homozygous ES5007 (Swed-homoz) brain was found to be approximately 62% of the level observed for mouse APP.

Under normal conditions, the proteolytic processing of mouse APP resulted in the generation of 5 C-terminal fragments. This contrasts with the pattern observed with Swedish-FAD m/hAPP where only the two largest C-terminal fragments were observed. The second largest C-terminal fragment (fragment 2) co-migrated with the LEC100 standard. The electrophoretic mobility of LEC100 was expected to closely resemble that of the C-terminal fragment released after the cleavage by beta-secretase. LEC100 consists of amino acid residues Leu, Gly, and Met juxtaposed with the beta-amyloid, transmembrane, and cytoplasmic domains of APP. spLEC100 (sp designates APP signal peptide, see below) was stably expressed in HEK293 cells (obtained from Sandra Reuter), a membrane homogenate prepared, and an aliquot was applied to the gel. In cells, LEC100 is generated after the signal peptide (sp) is proteolytically removed from spLEC100 during protein translation.

For other aspects of the nucleic acids, polypeptides, antibodies, etc., reference is made to standard textbooks of molecular biology, protein science, and immunology. See, e.g., Davis et al. (1986), *Basic Methods in Molecular Biology*, Elsevir Sciences Publishing, Inc., New York; Hames et al. (1985), *Nucleic Acid Hybridization*, IL Press, *Molecular Cloning*, Sambrook et al.; *Current Protocols in Molecular Biology*, Edited by F.M. Ausubel et al., John Wiley & Sons, Inc; *Current Protocols in Human Genetics*, Edited by Nicholas C. Dracopoli et al., John Wiley & Sons, Inc.; *Current Protocols in Protein Science*; Edited by John E. Coligan et al., John Wiley & Sons, Inc.; *Current Protocols in Immunology*; Edited by John E. Coligan et al., John Wiley & Sons, Inc.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The preceding preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The entire disclosure of all applications, patents and publications, cited below are hereby incorporated by reference.

From the foregoing description, one skilled in the art can easily ascertain the essential characteristics of this invention, and without departing from the spirit and scope thereof, can make various changes and modifications of the invention to adapt it to various usages and conditions.

Tables

Table I

Transgenic line	ES cell clone	Targeting vector	Gene Product	mAPP mutations
ES5007	B12	pMTI-2398	Swedish-FAD m/h APP	KM(670,671)NL; G(676)R; F(681)T, R(684)H
ES5103	C87	pMTI-2454	Swedish/London-FAD m/h APP	KM(670,671)NL; V(717)I; G(676)R, F(681)T, R(684)H
ES5215	A54	pMTI-2455	Swedish-FAD m/hAPP713	KM(670,671)NL; T(714)stop; G(676)R, F(681)T, R(684)H
ES5401	D12	pMTI-2453	London-FAD m/h APP	V(717)I; G(676)R, F(681)T, R(684)H
ES5403	D60	pMTI-2453	London-FAD m/h APP	V(717)I; G(676)R, F(681)T, R(684)H

Table II

Transgenic Line	Germline-Transmission	m/h APP mRNA	m/h APP Protein	Altered C-Terminal Processing
ES5007	yes	yes	yes	yes
ES5103	yes	n.d.	yes	yes
ES5401	yes	n.d.	yes	n.d.
ES5403	yes	n.d.	yes	n.d.

n.d.: not determined

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